

01997001800.ST25
SEQUENCE LISTING

<110> Liu, wei
Ozenberger, Bradley A.
Wu, Leeying
Lo, Ching-Hsiung Frederick
Haney, Steven A.
Sookdeo, Hemchand
Lee, Jee Hyung

<120> NOVEL BRAIN-LOCALIZED PROTEIN KINASES HOMOLOGOUS TO
HOMEODOMAIN-INTERACTING PROTEIN KINASES

<130> 01997.001800

<150> US 60/456,958
<151> 2003-03-25

<150> US 60/491,251
<151> 2003-07-31

<160> 191

<170> PatentIn version 3.2

<210> 1
<211> 1851
<212> DNA
<213> Homo sapiens

<220>
<221> CDS
<222> (1)..(1848)

<400> 1	48
atg tcc acc atc cag tcg gag act gac tgc tac gac atc atc gag gtc	
Met Ser Thr Ile Gln Ser Glu Thr Asp Cys Tyr Asp Ile Ile Glu Val	
1 5 10 15	
ttg ggc aag ggg acc ttc ggg gag gta gcc aag ggc tgg cgg cgg agc	96
Leu Gly Lys Gly Thr Phe Gly Glu Val Ala Lys Gly Trp Arg Arg Ser	
20 25 30	
acg ggc gag atg gtg gcc atc aag atc ctc aag aat gac gcc tac cgc	144
Thr Gly Glu Met Val Ala Ile Lys Ile Leu Lys Asn Asp Ala Tyr Arg	
35 40 45	
aac cgc atc atc aag aac gag ctg aag ctg ctg cac tgc atg cga ggc	192
Asn Arg Ile Ile Lys Asn Glu Leu Lys Leu His Cys Met Arg Gly	
50 55 60	
cta gac cct gaa gag gcc cac gtc atc cgc ttc ctt gag ttc ttc cat	240
Leu Asp Pro Glu Glu Ala His Val Ile Arg Phe Leu Glu Phe Phe His	
65 70 75 80	
gac gcc ctc aag ttc tac ctg gtc ttt gag ctg ctg gag caa aac ctt	288
Asp Ala Leu Lys Phe Tyr Leu Val Phe Glu Leu Leu Glu Gln Asn Leu	
85 90 95	
ttc gag ttc cag aag gag aac aac ttc gcg ccc ctc ccc gcc cgc cac	336
Phe Glu Phe Gln Lys Glu Asn Asn Phe Ala Pro Leu Pro Ala Arg His	
100 105 110	

01997001800.ST25

atc cgt aca gtc acc ctg cag gtg ctc aca gcc ctg gcc cg ^g ctc aag	384
Ile Arg Thr Val Thr Leu Gln Val Leu Thr Ala Leu Ala Arg Leu Lys	
115 120 125	
gag ctg gct atc atc cac gct gat ctc aag cct gag aac atc atg ctg	432
Glu Leu Ala Ile Ile His Ala Asp Leu Lys Pro Glu Asn Ile Met Leu	
130 135 140	
gtg gac cag acc cgc tgc ccc ttc agg gtc aag gtg att gac ttc gga	480
Val Asp Gln Thr Arg Cys Pro Phe Arg Val Lys Val Ile Asp Phe Gly	
145 150 155 160	
tcc gcc agc att ttc agc gag gtg cgc tac gtg aag gag cca tac atc	528
Ser Ala Ser Ile Phe Ser Glu Val Arg Tyr Val Lys Glu Pro Tyr Ile	
165 170 175	
cag tcg cgc ttc tac cgg gcc cct gag atc ctg ctg ggg ctg ccc ttc	576
Gln Ser Arg Phe Tyr Arg Ala Pro Glu Ile Leu Leu Gly Leu Pro Phe	
180 185 190	
tgc gag aag gtg gac gtg tgg tcc ctg ggc tgc gtc atg gct gag ctg	624
Cys Glu Lys Val Asp Val Trp Ser Leu Gly Cys Val Met Ala Glu Leu	
195 200 205	
cac ctg ggc tgg cct ctc tac ccc ggc aac aac gag tac gac cag gtg	672
His Leu Gly Trp Pro Leu Tyr Pro Gly Asn Asn Glu Tyr Asp Gln Val	
210 215 220	
cgc tac atc tgc gaa acc cag ggc ctg ccc aag cca cac ctg ttg cac	720
Arg Tyr Ile Cys Glu Thr Gln Gly Leu Pro Lys Pro His Leu Leu His	
225 230 235 240	
gcc gcc tgc aag gcc cac cac ttc ttc aag cgc aac ccc cac cct gac	768
Ala Ala Cys Lys Ala His His Phe Phe Lys Arg Asn Pro His Pro Asp	
245 250 255	
gct gcc aac ccc tgg cag ctc aag tcc tcg gct gac tac ctg gcc gag	816
Ala Ala Asn Pro Trp Gln Leu Lys Ser Ser Ala Asp Tyr Leu Ala Glu	
260 265 270	
acg aag gtg cgc cca ttg gag cgc cgc aag tat atg ctc aag tcg ttg	864
Thr Lys Val Arg Pro Leu Glu Arg Arg Lys Tyr Met Leu Lys Ser Leu	
275 280 285	
gac cag att gag aca gtg aat ggt ggc agt gtg gcc agt cgg cta acc	912
Asp Gln Ile Glu Thr Val Asn Gly Gly Ser Val Ala Ser Arg Leu Thr	
290 295 300	
ttc cct gac cgg gag gcg ctg gcg gag cac gcc gac ctc aag agc atg	960
Phe Pro Asp Arg Glu Ala Leu Ala Glu His Ala Asp Leu Lys Ser Met	
305 310 315 320	
gtg gag ctg atc aag cgc atg ctg acc tgg gag tca cac gaa cgc atc	1008
Val Glu Leu Ile Lys Arg Met Leu Thr Trp Glu Ser His Glu Arg Ile	
325 330 335	
agc ccc agt gct gcc ctg cgc cac ccc ttc gtg tcc atg cag cag ctg	1056
Ser Pro Ser Ala Ala Leu Arg His Pro Phe Val Ser Met Gln Gln Leu	
340 345 350	
cgc agt gcc cac gag acc acc cac tac tac cag ctc tcg ctg cgc agc	1104
Arg Ser Ala His Glu Thr Thr His Tyr Tyr Gln Leu Ser Leu Arg Ser	

01997001800.ST25

355

360

365

tac	cgc	ctc	tcg	ctg	caa	gtg	gag	ggg	aag	ccc	ccc	acg	ccc	gtc	gtg	1152
Tyr	Arg	Leu	Ser	Leu	Gln	Val	Glu	Gly	Lys	Pro	Pro	Thr	Pro	Val	Val	
370				375					380							
gcc	gca	gaa	gat	ggg	acc	ccc	tac	tac	tgt	ctg	gct	gag	gag	aag	gag	1200
Ala	Ala	Glu	Asp	Gly	Thr	Pro	Tyr	Tyr	Cys	Leu	Ala	Glu	Glu	Lys	Glu	
385				390					395					400		
gct	gcg	ggt	atg	ggc	agt	gtg	gcc	ggc	agc	agc	ccc	ttc	ttc	cga	gag	1248
Ala	Ala	Gly	Met	Gly	Ser	Val	Ala	Gly	Ser	Ser	Pro	Phe	Phe	Arg	Glu	
			405				410							415		
gag	aag	gca	cca	ggt	atg	caa	aga	gcc	atc	gac	cag	ctg	gat	gac	ctg	1296
Glu	Lys	Ala	Pro	Gly	Met	Gln	Arg	Ala	Ile	Asp	Gln	Leu	Asp	Asp	Leu	
			420			425						430				
agt	ctg	cag	gag	gct	ggg	cat	ggg	ctg	tgg	ggt	gag	acc	tgc	acc	aat	1344
Ser	Leu	Gln	Glu	Ala	Gly	His	Gly	Leu	Trp	Gly	Glu	Thr	Cys	Thr	Asn	
			435			440					445					
gcg	gtc	tcc	gac	atg	atg	gtc	ccc	ctc	aag	gca	gcc	atc	act	ggc	cac	1392
Ala	Val	Ser	Asp	Met	Met	Val	Pro	Leu	Lys	Ala	Ala	Ile	Thr	Gly	His	
			450			455					460					
cat	gtg	ccc	gac	tcg	ggc	cct	gag	ccc	atc	ctg	gcc	ttc	tac	agc	agc	1440
His	Val	Pro	Asp	Ser	Gly	Pro	Glu	Pro	Ile	Leu	Ala	Phe	Tyr	Ser	Ser	
			465			470					475				480	
cgc	ctg	gca	ggc	cgc	cac	aag	gcc	cgc	aag	cca	cct	gcg	ggt	tcc	aag	1488
Arg	Leu	Ala	Gly	Arg	His	Lys	Ala	Arg	Lys	Pro	Pro	Ala	Gly	Ser	Lys	
			485			490						495				
tcc	gac	tcc	aac	tcc	agc	aac	ctc	att	cgg	ctg	agc	cag	gtc	tcg	cct	1536
Ser	Asp	Ser	Asn	Phe	Ser	Asn	Leu	Ile	Arg	Leu	Ser	Gln	Val	Ser	Pro	
			500			505					510					
gag	gat	gac	agg	ccc	tgc	cgg	ggc	agc	agc	tgg	gag	gaa	gga	gag	cat	1584
Glu	Asp	Asp	Arg	Pro	Cys	Arg	Gly	Ser	Ser	Trp	Glu	Glu	Gly	Glu	His	
			515			520					525					
ctc	ggg	gcc	tct	gct	gag	cca	ctg	gcc	atc	ctg	cag	cga	gat	gag	gat	1632
Leu	Gly	Ala	Ser	Ala	Glu	Pro	Leu	Ala	Ile	Leu	Gln	Arg	Asp	Glu	Asp	
			530			535					540					
ggg	ccc	aac	att	gac	aac	atg	acc	atg	gaa	gct	gag	agg	cca	gac	cct	1680
Gly	Pro	Asn	Ile	Asp	Asn	Met	Thr	Met	Glu	Ala	Glu	Arg	Pro	Asp	Pro	
			545			550					555				560	
gag	ctc	tcc	gac	ccc	agc	agc	tgt	cct	gga	gaa	tgg	ctg	agt	gag	cca	1728
Glu	Leu	Phe	Asp	Pro	Ser	Ser	Cys	Pro	Gly	Glu	Trp	Leu	Ser	Glu	Pro	
			565			570						575				
gac	tgc	acc	ctg	gag	agc	gtc	agg	ggc	cca	cgg	gct	cag	ggg	ctc	cca	1776
Asp	Cys	Thr	Leu	Glu	Ser	Val	Arg	Gly	Pro	Arg	Ala	Gln	Gly	Leu	Pro	
			580			585						590				
ccc	cgc	cgc	tcc	cac	cag	cat	ggt	cca	ccc	cgg	ggg	gcc	acc	agc	tcc	1824
Pro	Arg	Arg	Ser	His	Gln	His	Gly	Pro	Pro	Arg	Gly	Ala	Thr	Ser	Phe	
			595			600						605				
ctc	cag	cat	gtc	acc	ggg	cac	cac	tga								1851

01997001800.ST25

Leu Gln His Val Thr Gly His His
610 615

<210> 2
<211> 616
<212> PRT
<213> Homo sapiens

<400> 2

Met Ser Thr Ile Gln Ser Glu Thr Asp Cys Tyr Asp Ile Ile Glu Val
1 5 10 15

Leu Gly Lys Gly Thr Phe Gly Glu Val Ala Lys Gly Trp Arg Arg Ser
20 25 30

Thr Gly Glu Met Val Ala Ile Lys Ile Leu Lys Asn Asp Ala Tyr Arg
35 40 45

Asn Arg Ile Ile Lys Asn Glu Leu Lys Leu Leu His Cys Met Arg Gly
50 55 60

Leu Asp Pro Glu Glu Ala His Val Ile Arg Phe Leu Glu Phe Phe His
65 70 75 80

Asp Ala Leu Lys Phe Tyr Leu Val Phe Glu Leu Leu Glu Gln Asn Leu
85 90 95

Phe Glu Phe Gln Lys Glu Asn Asn Phe Ala Pro Leu Pro Ala Arg His
100 105 110

Ile Arg Thr Val Thr Leu Gln Val Leu Thr Ala Leu Ala Arg Leu Lys
115 120 125

Glu Leu Ala Ile Ile His Ala Asp Leu Lys Pro Glu Asn Ile Met Leu
130 135 140

Val Asp Gln Thr Arg Cys Pro Phe Arg Val Lys Val Ile Asp Phe Gly
145 150 155 160

Ser Ala Ser Ile Phe Ser Glu Val Arg Tyr Val Lys Glu Pro Tyr Ile
165 170 175

Gln Ser Arg Phe Tyr Arg Ala Pro Glu Ile Leu Leu Gly Leu Pro Phe
180 185 190

Cys Glu Lys Val Asp Val Trp Ser Leu Gly Cys Val Met Ala Glu Leu
195 200 205

01997001800_ST25

His Leu Gly Trp Pro Leu Tyr Pro Gly Asn Asn Glu Tyr Asp Gln Val
210 215 220

Arg Tyr Ile Cys Glu Thr Gln Gly Leu Pro Lys Pro His Leu Leu His
225 230 235 240

Ala Ala Cys Lys Ala His His Phe Phe Lys Arg Asn Pro His Pro Asp
245 250 255

Ala Ala Asn Pro Trp Gln Leu Lys Ser Ser Ala Asp Tyr Leu Ala Glu
260 265 270

Thr Lys Val Arg Pro Leu Glu Arg Arg Lys Tyr Met Leu Lys Ser Leu
275 280 285

Asp Gln Ile Glu Thr Val Asn Gly Gly Ser Val Ala Ser Arg Leu Thr
290 295 300

Phe Pro Asp Arg Glu Ala Leu Ala Glu His Ala Asp Leu Lys Ser Met
305 310 315 320

Val Glu Leu Ile Lys Arg Met Leu Thr Trp Glu Ser His Glu Arg Ile
325 330 335

Ser Pro Ser Ala Ala Leu Arg His Pro Phe Val Ser Met Gln Gln Leu
340 345 350

Arg Ser Ala His Glu Thr Thr His Tyr Tyr Gln Leu Ser Leu Arg Ser
355 360 365

Tyr Arg Leu Ser Leu Gln Val Glu Gly Lys Pro Pro Thr Pro Val Val
370 375 380

Ala Ala Glu Asp Gly Thr Pro Tyr Tyr Cys Leu Ala Glu Glu Lys Glu
385 390 395 400

Ala Ala Gly Met Gly Ser Val Ala Gly Ser Ser Pro Phe Phe Arg Glu
405 410 415

Glu Lys Ala Pro Gly Met Gln Arg Ala Ile Asp Gln Leu Asp Asp Leu
420 425 430

Ser Leu Gln Glu Ala Gly His Gly Leu Trp Gly Glu Thr Cys Thr Asn
435 440 445

Ala Val Ser Asp Met Met Val Pro Leu Lys Ala Ala Ile Thr Gly His
450 455 460

01997001800.ST25

His Val Pro Asp Ser Gly Pro Glu Pro Ile Leu Ala Phe Tyr Ser Ser
 465 470 475 480

Arg Leu Ala Gly Arg His Lys Ala Arg Lys Pro Pro Ala Gly Ser Lys
 485 490 495

Ser Asp Ser Asn Phe Ser Asn Leu Ile Arg Leu Ser Gln Val Ser Pro
 500 505 510

Glu Asp Asp Arg Pro Cys Arg Gly Ser Ser Trp Glu Glu Gly Glu His
 515 520 525

Leu Gly Ala Ser Ala Glu Pro Leu Ala Ile Leu Gln Arg Asp Glu Asp
 530 535 540

Gly Pro Asn Ile Asp Asn Met Thr Met Glu Ala Glu Arg Pro Asp Pro
 545 550 555 560

Glu Leu Phe Asp Pro Ser Ser Cys Pro Gly Glu Trp Leu Ser Glu Pro
 565 570 575

Asp Cys Thr Leu Glu Ser Val Arg Gly Pro Arg Ala Gln Gly Leu Pro
 580 585 590

Pro Arg Arg Ser His Gln His Gly Pro Pro Arg Gly Ala Thr Ser Phe
 595 600 605

Leu Gln His Val Thr Gly His His
 610 615

<210> 3
 <211> 14317
 <212> DNA
 <213> Homo sapiens

<400> 3		
gagttgaggt tttgtcatgt tggcaaggct ggtctcaaac tcctgaccc tc aggtgatccg	60	
cccaccttgg cctctcaaag tgctggatt acaggcgtaa gccaccactc ctggccaggc	120	
actttaaaaa cttctttgtg ctttgatttt ctcttccata aaatccctac tttgtatgtt	180	
gtaaggatca gataagactt ctaaagaact tcatccttgt ttaaatgttt tgatgttaca	240	
ttttctttta cttttttttt tttttttgag acggagtttc actcttggcc cccaggctgg	300	
agtgcattgg cgcaatcttg gctcactgca accccaccc tc cgcgttcaa gcagttctca	360	
tacctcagcc tgccgaccc tc agcctttga gtagctggga ctacaggcat gtgctaaca	420	
acccggctaa ttttgtatgtt ttagtagaga cggggtttctt ccatgttggc caggctggc	480	

01997001800.ST25

tcgaactccc	gacctcaggt	gatccacctg	cctcagcctc	ccaaagtgtct	gggattacag	540
gcatgagcca	ccgagcccg	cccgctgtta	aatattctaa	tctggctgga	gtggtggctc	600
atgtctacaa	tcccagcact	ttggaagggtt	gaggcaggag	gatcacttga	ggccaggagg	660
atcacttgag	accagcctgg	acaacatagt	gagacccat	ttctacaaaa	aattaaaaag	720
ataaaataaaa	atgaacactt	ttttttttt	tttgagatgg	agtctcgctc	tgtcacccag	780
gctggagtgc	agtggtgcaa	tctcggtca	ctgcaacctc	cacctccgg	gttcaagcta	840
ttcttctgcc	ttagcctccc	gagtagctgg	gactacaggc	gccctccact	atgcctggct	900
aatttttagt	attttttagta	gagacagagt	ttcaccgtgt	tagccaggat	ggtctcgatc	960
tcctgacctt	atgatctgcc	ttccttggcc	tcccaaagtg	ctgggattac	aggcgtgacc	1020
caccgcaccc	agccaaaaat	aaatacattt	tctaatttg	cctcaacatc	tcccccaagc	1080
tgcttcttat	ccatgtccat	ttctcgggga	ctgccccttc	atcccagagc	cctaggcccg	1140
ttcttagaca	gctcccgcct	ttccctcaaa	ccgtcggtct	cacggctgct	tctcctggcc	1200
ttttgagtgt	ctcatccatt	ggcctcgccc	tctcctcccc	aacctctccc	atctgtgccc	1260
tgtcctggac	tctttccctg	gcttgggct	tccactctta	cccgctccaa	cctatccctt	1320
ttcatacagt	aacttctga	cactcatatc	tgaccctgcc	ctcccctgct	caaagccctt	1380
ctgtggctcc	ccagtgcct	cagaacagaa	tccaaactcc	ttagcctggc	attcagggcc	1440
ttttacaacc	tcaccccaaca	gtagccacag	actgggacag	gagtttctg	aacacagaca	1500
cacacacatc	acatctcca	agctcaagaa	gcccacctt	cctcaactcct	gccttatccc	1560
cattcctgta	tgcccaaggc	ccacgattag	accccccctt	gtcaacactt	cacctgtttg	1620
gtcttgcaa	gattccgcca	ctggcgggg	gagggggccc	agctggta	cccacccca	1680
ctccagccag	ggctcaggc	tccaacaaca	gaaccagagc	cactcaacag	cgctggaacc	1740
cattcggtgg	ggcctggggc	ccctcatccc	aagccaggag	ggtttctggg	gaggggtgca	1800
gccccctggca	gactgacagt	gtggcctggg	ggtttgggg	tgccaggaa	gcaggggcc	1860
acctcatagg	aggagacacg	agtgcggttc	tctttcccc	actggggggc	ctgctgtgtc	1920
agcagccagg	cgggaggcct	gggcggcaga	gccagtggta	cagggccctg	ggcagggcgg	1980
tgtctggcag	cagcggcacc	atgtccacca	tccagtcgga	gactgactgc	tacgacatca	2040
tcgaggtctt	gggcaagggg	acttcgggg	agtagccaa	gggctggcgg	cgagcacgg	2100
gcgagatggt	ggccatcaag	atcctcaaga	atgacgccta	ccgcaaccgc	atcatcaaga	2160
acgagctgaa	gctgctgcac	tgcacgcgag	gcctagaccc	tgaagaggcc	cacgtcatcc	2220
gcttccttga	gttcttccat	gacgccctca	agttctacct	ggttttgag	ctgctggagc	2280
aaaacctttt	cgagttccag	aaggagaaca	acttcgcgcc	cctcccgcc	cgccacatcc	2340
gtacagtcac	cctgcagggt	ctcacagccc	tggcccgct	caaggagctg	gctatcatcc	2400

01997001800.ST25

acgctgatct caagcctgag aacatcatgc tggtggacca gaccgctgc cccttcaggg	2460
tcaaggtgag taggggtcgt ctagggtggc tgcgtcccta gttccttgc ttttcccag	2520
cttcttcag ccctagattt ttttttaat tttttaaaat tattattatt attattttg	2580
agacggagtt tcattctgtt acccaggctt gagtgcagtg gcgcaatctc agtcactgc	2640
aactccgcct cctgggttca agtgattatc ctgcctcagc ctcccagtt gctgggatta	2700
cagggatgcg ccaccacgcc cagctaattt ttttttgc tttatcagag acggggtgat	2760
gatggcatga tcttgggttca ctgcctccgc ctcccggtt caagcgattc tcctgcctca	2820
gcctcctgag tagctggaa tacaggtgcc cgccaccat gcccggctaa tttttgtatt	2880
tttagtagag atggggtttc gccatgttgg ccaggcttgtt ctcaaactcc tgaccttgt	2940
atccacactgc ctcagcctcc caaagtgctg ggattacagg cgtgagccac cacgcccagc	3000
caattttgt gtttttgggt agaaacagga tttcatcatg ttgcccaggc tggctcaaa	3060
gtcctgagtt caagcaatct gcccaccttgc gcctcaacaa agtgcgtggaa ttacaagtgt	3120
gagccaccat gcccagtcttgc ctgtctgttgc ttgagtttga tactgtctgg atgcttctga	3180
accagggca ccctgagggc aaggctgggg ctgacttaat catcgctgtg tccctgacat	3240
ctcccagcac tgcagtcatg gagccagtgc taaatgaatg cttgcccagag acacagagac	3300
agaaaaaaggt ggattattct gccccaaagag gtggaaggac agagacccag ggaagcaggg	3360
acttccacaa acacagcagg ggacagacag gacggatcca cagcacctgg ccggcattat	3420
caccccaact gtctctgtgg aaggaatgaa ttcattccac aaacatagac taagtgcacca	3480
gggtcaactca gcctcttggg tactgaagcc ctggcactct gggatcagaa tagcaattaa	3540
taaccatttc atgatactgc tttctgcaag taaaaggta gggatggcca ggtgcgggtgg	3600
ctcacgcctg taatcccagc actttggag gccgaggcgg gtggatcacc tgaggtcagg	3660
agttcaagac cagcctgacc aatatggta aacctcgctc ctgctaaaag tataaaaatt	3720
agccgggtgt ggtggcgggc acctgtaatc ctgactactc cagaggctga agcagataaa	3780
tcgcttagaa cccgggaggc agaggttgca gtgagctgag attacgcac tgcactccag	3840
cctggcgcac agaggaagtgc cctctgtctc agaaaaaaaaaaa ctaaactaaa	3900
attagctagg cgtggtggca catacctgga atcccgatgtt gttggggggc agaggcagga	3960
gactcaacttgc aacttggag gcagaggttt tgcagtgc ttagatcactc ccactgcact	4020
ccagcctggg cgacagagct cgactctgtc tcaacacaaa acaaaaaacaa aaaactgaga	4080
aatggctgaa taaaaggcag aaaaactcag agaaggaaac aggctggcca ggtgtgggtgg	4140
cccaagcctg taatcccagc actttggag gctgaggcag gtggatcacc tgaggtcaga	4200
agctcaagac cagcctggcc aacatggta aatcctgtct ctataaaaa tacaaaactt	4260

01997001800.ST25

agccagatgt ggtgggtgc acctgtaatc ccagctactt gggaggctga tgcaggagaa	4320
tcgcttgaac ccatatgggg gcggagggtt cagtgagccg agatcatgcc gctgcactcc	4380
agcttggaca aaagagtcaa gccacctgaa aaagaaaaag aaaaagaaac aggccaagag	4440
agagtcacgg agattcaggg tgaaaatggc agacagctcc accagaggca tggggagaga	4500
caaaggctt cggccattcg caatgttggt tccgcagctg ttggccaagc acctgtcatg	4560
tgtcaaaggc ctgtgacgag tgtaacagt gcctgaagag gaagacagaa gaggaccggg	4620
acttcaggg a ggtgtcttcc tagtggacga cacagagaca gagatggaaa gagagagaga	4680
gacactgaga gacaagagac aggcaagtga tggagaggca gttgcaaaga aagaacgaga	4740
ggtacaaatg gccaggcaca gtggctcatg cctagaatct caggacttg ggaggccgag	4800
gtgggaggat tactagagcc caggagttca agaccagcct gggtaacatg gtgaaaaccc	4860
atctctacta aaaatacaa aattagccgg gcatggtgc atgtgactgt agtcccagct	4920
acttgggagg ctgaggcagg agaatcgctt gaacgtggaa ggtggaggtt gccttgagcc	4980
gagattgcgc cactgcattc cagcctgggt gacagggtga gccactgtct caaatgagag	5040
acagagagag agagatacaa gcaagagatg gaaagagaat gaaggaactc aaagcccata	5100
catacattca ttcatttact cattatttac tgagccctg ctgtgtgcca agccctgttc	5160
taggcattca gggatacagt attgaacaaa atggataaat tctttgcct cgtggactg	5220
acatcctcgc tggggagaga aatgctgaga gaggccaggt gcagggccctc atgcctataa	5280
tcccagcatg ttgggaggct gaggcaggag gatcactga gcccaggagc catcctggc	5340
aacatagtga gacccatctc tatctctaca aaaagttaaa aaattagctg ggtatggagg	5400
tgcattgcctg tggcccagc tactcaggag gctgaggcgg gaggatctt tgagccctgg	5460
agttcgcggc tacagtgagc tacatgggt ccactgtact ccagcctggg tgatagagca	5520
agaccctgtc tctaaaaagg aaaaaaggc tggcgccgt ggctcacgcc tgtaatccca	5580
acactttggg aggctgagggc gggcagatca tctgagtcag gagttgaga ccagcctggc	5640
taacatggtg aaaccccgcc tgtctctacc aaaaatgcaa aagattagcg cttgtatcc	5700
cagctactca ggaggcttag gcaggagaat cactgaaatc cagtaggtgg aggttgcagt	5760
gagccaagat cacaccactg ctctccagcc tggccaacag agcgagactc cgtcacaaaa	5820
aaataaataa taaaaataa aaattaaaat aaaaaattaa gagatatagt gtgtgaaatg	5880
gcattaaagag caatggtgaa cctgggtgcg gtggctcacg cctgtcctag cactttggga	5940
ggccgaggcg agtggatcac ctgcggtcag gagttcgaga ccagcctggc catcatcg	6000
aaaccccgtc tctactaaaa atataaaaat tagctgcgc tgggtgtgtg cacctgtaat	6060
cccagctact tgggaggctg aagcaggaga atcactggaa cctgggagga ggaggttgca	6120
gtgagccaag attgcaccat tgcactccag cctgggtgac aagagcaaaa ctctgtctca	6180

01997001800.ST25

aaaacctccg	actcaaaaaa	aaaaaaaaaa	aaaaaaaaaa	gaaaagaaaa	gaaaagaaaa	6240
aacaggggcc	tggccgggga	tagaaaggat	ggggactgat	ggctgatgct	ttcacagaat	6300
gattaggaa	ggtctcactg	agaaggtgat	cattttttt	tgtcctgcct	ttcacccccc	6360
gatagaaagg	tgacattga	gtaaagacct	gaaggaggtg	aggcagggag	ccctgtgctc	6420
atgcagggaa	gagcattcca	ggcagaggga	acagcgagt	caaaagccct	gagctggaa	6480
tgtctgactt	gttcaaggaa	tagtgaggag	acccttgcgg	ctggaggagg	gtgagtgtat	6540
gggagagtgg	gagatgtggc	agagaggta	cagagcagac	attggagacc	tgtggccac	6600
ggtgaggact	ttggctttt	tcacaggat	tggctatgag	caggggagga	cccaatctat	6660
cccgccggc	cacaggatcc	ctctggatgc	ttgtgacaga	cagactaggg	ggcagaggag	6720
aggagcaggg	agaccagcga	ggagaccccc	gcgttggct	agtttgaaa	ggatgcagga	6780
taggaccagg	gtcggggctg	tggatggcat	gcagaggag	cagattctag	atctgttggc	6840
tgtatggacaa	ggtgtggggt	gcaagaggaa	gagtagggtc	ctaaccctcc	tttgcatagt	6900
tctatggag	agaaacacag	acagagtca	tcactcgaac	cagacacaaa	ggctggaaaga	6960
gacagagata	gggacttaac	aactacggcc	acagctgggt	gcggtggctc	atgcctgtaa	7020
ttccacact	tagggaggt	gaggaggca	gatcatctga	ggtcaggagt	ttaagaccag	7080
cctggccaac	agggtgaaac	cccgctcta	ctaaaaatac	aaaaattagc	agggcatgg	7140
gggtgtcacc	tgttagacca	gctattcagg	agactgaggc	tggagaatca	cttgaaccca	7200
ggaggcagag	gttgcata	gccaagattg	cgccactgca	ctttagcctg	ggcgacagag	7260
ttagactcgg	tctcaaaaaa	aaaaaaaaaa	ccaacaaagg	ctgggtgcgg	tggctcacgc	7320
ctgtatccc	agcactttgg	gaggccgagg	cgggtgggtc	acatgaggc	aggagttcga	7380
gaccagcctg	gccaacatag	tgaaacccca	tctctactaa	aaatacaaaa	aattagccgg	7440
gtgtgggtgt	gggcgcctgc	aatcccagct	actcaggagg	ctaaggcagg	agaatcgctt	7500
gaaccgggaa	ggtggaggtt	gcagtgtgc	gagatcgtgc	cattgcactc	cagactggc	7560
aacaagagt	agactctgtc	tcaaacaac	aaacaaacaa	acaacaaaaa	accaacaaag	7620
caactaaaga	atcacagacc	cagagatggc	cagagtcaa	tagcagatgc	aggaagatgc	7680
caggtgaaag	atgccggggt	ggcccgctc	ggctgtccct	gctgcttgac	ctgcccactc	7740
gccctttcc	ccaccccccga	caggtgattg	acttcggatc	cgccagcatt	ttcagcgagg	7800
tgcgtacgt	gaaggagcca	tacatccagt	cgcgcttcta	ccggggccct	gagatcctgc	7860
tggggctgcc	cttctgcgag	aaggtggacg	tgtggccct	gggctgcgtc	atggctgagc	7920
tgcacccctgg	ctggccctc	tacccggca	acaacgagta	cgaccagg	cgctacatct	7980
gcgaaaccca	gggcctgccc	aagccacacc	tgttgcacgc	cgcctgcaag	gcccaccact	8040

01997001800.ST25

tcttcaagcg caaccccccac cctgacgctg ccaacccctg gcagctcaag tcctcggtcg 8100
actacctggc cgagacgaag gtaaggaaa agttgggtga gggcagtcag tgtggggct 8160
gttacatgaa aaaaattct agggtggca acgtggctca caccgtaat tccagcactt 8220
tgggaggctg tgggtggagg atcccttgag cctaggggtt tgagaccagc ctggggaca 8280
tagtgagacc tcctctttat aaaacatgga aaaaaaaatc agctggcac ggtggatgg 8340
gcctattgtc ccagatacat gggaggctga ggcaggagaa ttccttgagc ctgggaggtc 8400
caggctacag tgaactatga tcatgccact acacttgagc ctgggtgaca gagcaagact 8460
ctgtttcaaa aagaaaaatc tatcagacca gaagaatgga gtgaaaagaa caaaaaacag 8520
aggctgggtg tgggtggctta cgccctgtaat cccagcactt tggagtcg aggtgggtgg 8580
atcacgaggt caggagttt agaccagcct ggccaagatg atgaaaccca gtctctacta 8640
aaaacacaaa aaattagctg ggccgagtgg cagacgcctg taattccagc tactcggcgg 8700
gctgaggcag gagaatcgct tgaacccaga gggcggaggt tgcagtgagc cgagatccca 8760
ccactgcact ccagcctggg caacagagtg agactccgtc tcaaaaaaaaaa aaaaaaaaaa 8820
gaaagaaaag aaaaatattt ttttttttt ttttaagac ggagtcttga tctgttgctc 8880
aggctggagt gcagtggtgc ggtctcagct cactgcaacc tctgcctccc aggttcaaga 8940
gattccctg cctcagcctc ctgagtagct gggcttacag gcacccacca tcacacccgg 9000
caattttttt gtattttac tagagacggg gtttaccat gttggccagg ctggtctcag 9060
acacccgacc tcgtgatcca cccacctcga cctcccaaag cagttagatt acaggcatga 9120
gccaccgcgc tcggccaaaa aaatattttt ttaataattt aaaaaaaaaa tttctgggct 9180
aaacctcaat gaggactgga acttgggggt cagccttaggg cattttcaca gcaagaaaga 9240
gctgcatgag atcaaatgtg ggactggtca gcaactgcag caagatagat ctgggggaga 9300
aactgcaggg agaatttagat gtttggaaat cagatgtggg ggctgctcta gcaagagaga 9360
tctgggtcat actataatgt tgacaggacg attggggcag cttctctgcc agttcagct 9420
ccggggtcag caacttgtgt ggcaagaggg attagaccac agagaatata tgaggtctga 9480
gattggctat gagaattgcg agagaggcca ggtgcagtgg cttatgcctg tagtccacgc 9540
actttggtgg gggccaaggc aggaggatca cttgaagtca ttgtggcga catagcaaga 9600
ctgtgtctt agaaaaattt tttttaaaa tttagccagg catggtggca cacaccgta 9660
gttccaagct acttgggagg ctgaggtggg aagatcactt gaacccagga gttggcagtt 9720
gcagtgagct atgattgcac cactacaccc cagtctggc gacacagcaa gaccctgttt 9780
aaaaaaaaagg atctaaggcc aggcacagtg gctcacacct gtaatcccag cactttggga 9840
ggccgaggtg ggtggatcac ctgaggtcag gagttcgaga acagcctggc caacatggtg 9900
aaaccccatc tctactaaaa atacaaaaat tagctggca tgggtggatggc cacctgtaat 9960

01997001800.ST25

tccagctgct caggaggctg aggaggaga atcgcttcaa cctgggaggt ggaggttgca	10020
gtgagccgag attgtaccac tgcactccag cctgggcaac aagagtaaa ctctgtctca	10080
cacacataca aaaaaaaaaa aaaaaaaaaa aaaaaaaaaaagg gatctgagtg agacccagg	10140
ttagtctaga gtttgggc agcagccagt ctgctacctc tgtggcttgc cccctccat	10200
ctgtcagca agagcctggg ttagacagca gaggggacta ggagttttag gtcataagg	10260
ttgatttcac agcaagaagg gtctggatgg gaccacaggt gagactaaaa gtcaatggca	10320
gtttaatagc aggggggtgac aaactactat agcaagaagg gtctgggtt gaccaccagg	10380
aggcctggga tcaagtgtgg agctgtggca gtaagaggga cctggatttgc attccagg	10440
ggactagaga ttccgggcag cccttctgct agctgtggt aggggctgca cccatggtgc	10500
tgaaggggac tggaggtctg gggcaagggg tggaaacttgg gccagtgtt tgggttcgat	10560
tagaggggct tgggtgtgac ggatccaggg tggccctcct agcagccaga gagctccaag	10620
gcagatcatg ggcagacctg gaagtcgggg ctacatgtgg gtgccacagc aggagtgc	10680
agggccctag ccctgcacaa tggtaaccc tgcccccttc tccatgcccc gccagg	10740
cccatggag cgccgcaagt atatgctaa gtcgttgac cagattgaga cagtgaatgg	10800
tggcagtgtg gccagtcgac taacccccc tgaccggag ggcgtggcgg agcacccg	10860
cctcaagagc atgggtggagc tgatcaagcg catgctgacc tggagtcac acgaacgcat	10920
cagccccagt gctgccctgc gccacccctt cgtgtccatg cagcagctgc gcagtgc	10980
cgagaccacc cactactacc agctctcgct ggcgcgtac cgcctctgc tgcaagtgg	11040
gggaaagccc cccacgccc tcgtggccgc agaagatggg accccctact actgtctgg	11100
tgaggagaag gaggctgcgg gtatggcag tgtggccggc agcagccct tctccgaga	11160
ggagaaggca ccaggtatgc aaagagccat cgaccagctg gatgacctga gtctgcag	11220
ggctggcat gggctgtgg gtgagacctg caccaatgcg gtcctcgaca tgatggccc	11280
cctcaaggca gccatcactg gccaccatgt gcccgcgtc ggcctgagc ccattctgg	11340
cttctacagc agccgcctgg caggcccca caaggccgc aagccacctg cgggttccaa	11400
gtccgactcc aacttcagca acctcattcg gctgagccag gtctcgctg aggatgacag	11460
gccctgccc ggcagcact gggaggaagg agagcatctc gggccctcg ctgagccact	11520
ggccatcctg cagcgagatg aggtggcc caacattgac aacatgacca tggaaagctga	11580
ggtgagccgg gtgcgttcag gatacgatta gggtgggagg aggctcagca cacactcacc	11640
cgtgctcagg atatgattag tgtgtgagga ggctcaacac acactcaccc atgttcagga	11700
tacaattagg gacttaggag gtcagcaca cacctaatac cgtcaagata tgataagg	11760
cagcacttac ttagctactt ccaggctgtg acaaaaaactc agggcacagt aatctactt	11820

01997001800.ST25

taagaagctt gataaagagc ctggcaaca tagtgagatc ccgtctgcac caaaaaatta 11880
 gaaatattag ctggtttgg tggcatgcac ctgtagtcgg agctactcag gaggctgagg 11940
 tgggaggatc acttgagcca gggaggtcga ggctgcagtg agctgtcattt acatcactac 12000
 aaaggggcaa taaaggccca gcactggtaa gaccctagca catgctcacc ctcattcagga 12060
 ggaggtgaca gaggctcagc agacactaat acactaacac tgcttggctg atgcccctct 12120
 ctcttccccc acagaggcca gaccctgagc tcttcgaccc cagcagctgt cctggagaat 12180
 ggctgagtga gccagactgc accctggaga gcgtcagggg cccacgggct caggggctcc 12240
 caccggccg ctcccaccag catggtccac cccgggggc caccagcttc ctccagcatg 12300
 tcaccggca ccactgtatgg tgattccacc cctgcccattt actggggctg gcgttagctg 12360
 ggctggcatt ccctcccaac ctgaactgct cctcagagcc atctcctgaa cccacaaattt 12420
 attcttacag aaagatagtt atccagaaat tctcattccc cgtctgcgtt gcggtgcgtg 12480
 cctgcacacc tctcctaaac acagcagggc tttggagtct ggcccatgct cttggccag 12540
 aaggacagca ggaaaggggg ctgcaccccg ctggccctgc gctgcccctt ggccctgctg 12600
 cctctgtcta tttcaatata gaactgttca gcagtccctgc ttcaagcctg ctctcactgc 12660
 ctggggcttg gactggccct gggggaaatg ggggctccag gctggcaccc agtgcattgc 12720
 tctgcgtgc tggggccagc tgaccactgg cttaggcggg agcctggct gctgtcacac 12780
 taggaggaa aagctgtgct tgggtgacta acccttgccc taaatacgct atgtgcttgg 12840
 cgtgtggaa atccacccctc agaacatgct gtgttgcgtt tgggttataatc aagtttgcgg 12900
 gatgctgggg tctccttgc tgggtgacttgc tccttcctac atgtttacag gttggcatg 12960
 cactcaccca catttggac gtgctgggtg taaatccact tggcaggcct aaattcacac 13020
 ttgggtgcaca ctctggtgc cagccatgct tgggtgcgtt tggatgtgg caatggtttgc 13080
 gtccctgctg atcaatctgg gaacatgctt ctctgcagca catacccatg ctggctacat 13140
 gagtgctaag tccatgcccgg gccacagggt ggcacgcgtc atgctcagca caggtcagcc 13200
 catgtacact acatgttaag ggctcagcac atgccaaccc atgcccagcac atgctgaggg 13260
 ctcagtacat gctaacccac actggtcaca cactgagggc tcagcacatg ccagtgcacat 13320
 gttgagggt cagcacaaaa agatgtcccc accagaggcc catgcccgtt gtcccctacc 13380
 cctgcacccc atctcacacc actcagtcag gcacaggctg tacagacaag ttatttactt 13440
 attataaccc tggccctttt ttgcccggaa aagtgggggt gggccagggg gccaggccca 13500
 gcatgcaccc ccatttctttt gggggctgtat ccctccccca gctctgcgtgg gtcccggggc 13560
 cacagcgtca ggccgggtggg ggtggaggta gaggtggggag agcaggggag agagcctgag 13620
 gagccacaat gggcagaca gaagcggggg cgccgggaca gggaccgtga cccagagcac 13680
 ctgggtccgc gggggcccaag caggccttgg cctgcccact ggatcgggcc tcagagcagg 13740

01997001800.ST25

cggcaggcgt tgcccacgct gtcagctgag gtgtcaaggt catggctgta aggggagtcc 13800
 cagtcctca gaaaaatggc ctccagctgg ctccgcaggc cgcccctccc attctgcgtc 13860
 accagcagcg aggtgcccgc cgtctccgtg aagtagttgc cagaccagtt ggaggttcct 13920
 agagaggaat gggtggagca taagggcacc ctcggggggc cgcccctggt gtctgaaccc 13980
 cctcttcttc agcgccccgt ggtgctcaag acactcaccg atgttaggtgg cgcgttcagt 14040
 caccatgtac ttgttgtggt tgacacgggc atatgggatt cgagcctggg cctcatccgc 14100
 ggggaccaca aagagtttct gagtgggagg ggaggatggg aaggagtgtg agaggcaggg 14160
 ggagtcggag gagccccggg atcagggagc agagtgtgga gcgagatctg tggactcca 14220
 ctgctccca cagaatcctc gggggccaga acagggccag gtggaggggc cctctgagaa 14280
 cgaaagctga aagggaggcc ccgggtggtct catttgc 14317

<210> 4
 <211> 1851
 <212> DNA
 <213> *Mus musculus*

<220>
 <221> CDS
 <222> (1)..(1848)

<400> 4
 atg gcc acc atc cag tca gag act gac tgc tac gac atc att gaa gtt 48
 Met Ala Thr Ile Gln Ser Glu Thr Asp Cys Tyr Asp Ile Ile Glu Val
 1 5 10 15
 ctg ggc aag ggc act ttt gga gag gtg gcc aag ggc tgg cgt cgg agt 96
 Leu Gly Lys Gly Thr Phe Gly Glu Val Ala Lys Gly Trp Arg Arg Ser
 20 25 30
 aca ggt gaa atg gtg gcc atc aag atc ctg aag aac gat gcg tac cga 144
 Thr Gly Glu Met Val Ala Ile Lys Ile Leu Lys Asn Asp Ala Tyr Arg
 35 40 45
 agc cgc atc atc aag aat gag ctg aag ctg ctg cgc tgc gtg cga ggc 192
 Ser Arg Ile Ile Lys Asn Glu Leu Lys Leu Leu Arg Cys Val Arg Gly
 50 55 60
 ctg gac cct gac gag gcc cac gtt atc cgc ttc ctt gag ttc ttc cac 240
 Leu Asp Pro Asp Glu Ala His Val Ile Arg Phe Leu Glu Phe Phe His
 65 70 75 80
 gat gcc ctc aag ttc tac ctg gtc ttc gag ctt ttg gag caa aac ctc 288
 Asp Ala Leu Lys Phe Tyr Leu Val Phe Glu Leu Leu Glu Gln Asn Leu
 85 90 95
 ttt gag ttc cag aaa gag aac aac ttc gca ccc ctt cct gcc agg cac 336
 Phe Glu Phe Gln Lys Glu Asn Asn Phe Ala Pro Leu Pro Ala Arg His
 100 105 110
 atc cgc acg gtc aca ctg cag gta cta aga gcg ctg gcc cgg ctc aag 384
 Ile Arg Thr Val Thr Leu Gln Val Leu Arg Ala Leu Ala Arg Leu Lys

01997001800.ST25

115

120

125

432

gaa ctg gcc atc atc cac gct gac ctc aag cct gaa aac att atg ttg
 Glu Leu Ala Ile Ile His Ala Asp Leu Lys Pro Glu Asn Ile Met Leu
 130 135 140

480

gta gac cag acg cgc tgc ccc ttc agg gtc aag gtg atc gac ttt ggc
 Val Asp Gln Thr Arg Cys Pro Phe Arg Val Lys Val Ile Asp Phe Gly
 145 150 155 160

528

tcg gcc agc ata ttc agt gag gta cgc tat gtg aag gag cct tac atc
 Ser Ala Ser Ile Phe Ser Glu Val Arg Tyr Val Lys Glu Pro Tyr Ile
 165 170 175

576

cag tcc cgc ttc tac agg gcc cca gag atc ctg ctg ggg ctg ccc ttc
 Gln Ser Arg Phe Tyr Arg Ala Pro Glu Ile Leu Leu Gly Leu Pro Phe
 180 185 190

624

tgt gag aag gtg gac gtg tgg tct ctg ggc tgt gtc atg gcc gag cta
 Cys Glu Lys Val Asp Val Trp Ser Leu Gly Cys Val Met Ala Glu Leu
 195 200 205

672

cat ctg ggc tgg cct ctc tac cca ggc aac aat gag tat gac cag gtg
 His Leu Gly Trp Pro Leu Tyr Pro Gly Asn Asn Glu Tyr Asp Gln Val
 210 215 220

720

cgc tac atc tgt gag acc cag ggc tta ccc aag ccc cat ttg ctg cat
 Arg Tyr Ile Cys Glu Thr Gln Gly Leu Pro Lys Pro His Leu Leu His
 225 230 235 240

768

gcg gct cgc aag gct cac cac ttc ttc aag cgt aac ccc cac ccc gat
 Ala Ala Arg Lys Ala His His Phe Phe Lys Arg Asn Pro His Pro Asp
 245 250 255

816

gcc acc aac ccc tgg cag ctg aag tcc tct gct gac tac cta gct gag
 Ala Thr Asn Pro Trp Gln Leu Lys Ser Ser Ala Asp Tyr Leu Ala Glu
 260 265 270

864

acc aag gta cgt cct ctg gag cgc cgc aag tac atg ctc aaa tcc ttg
 Thr Lys Val Arg Pro Leu Glu Arg Arg Lys Tyr Met Leu Lys Ser Leu
 275 280 285

912

gac cag att gag aca gtg aat ggt ggt gga gct gtg agc cgg ctg agt
 Asp Gln Ile Glu Thr Val Asn Gly Gly Ala Val Ser Arg Leu Ser
 290 295 300

960

ttt cca gac cgg gag gcc ctg gcg gaa cac gca gac ctc aag agc atg
 Phe Pro Asp Arg Glu Ala Leu Ala Glu His Ala Asp Leu Lys Ser Met
 305 310 315 320

1008

gtg gag ctg atc aaa cgc atg ctg aca tgg gag tcg cac gaa cgc atc
 Val Glu Leu Ile Lys Arg Met Leu Thr Trp Glu Ser His Glu Arg Ile
 325 330 335

1056

agt ccc agt gcg gcc ctg cgt cac ccc ttc gtg tcc atg cag cag ctg
 Ser Pro Ser Ala Ala Leu Arg His Pro Phe Val Ser Met Gln Gln Leu
 340 345 350

1104

cgg agt gcc cac gag gcc acc cgc tac tac cag ctg tcg ctc aga ggc
 Arg Ser Ala His Glu Ala Thr Arg Tyr Tyr Gln Leu Ser Leu Arg Gly
 355 360 365

1152

01997001800.ST25

Cys	Arg	Leu	Ser	Leu	Gln	Val	Asp	Gly	Lys	Pro	Pro	Pro	Pro	Val	Ile	
370					375					380						
gcc	agc	gca	gag	gac	ggg	cct	ccc	tac	tac	cgc	ctg	gct	gag	gag	gag	1200
Ala	Ser	Ala	Glu	Asp	Gly	Pro	Pro	Tyr	Tyr	Arg	Leu	Ala	Glu	Glu	Glu	
385					390					395						400
gag	act	gca	gac	ctg	ggt	gtg	aca	ggc	agt	ggg	tcc	tcc	tcc	agg		1248
Glu	Thr	Ala	Gly	Leu	Gly	Gly	Val	Thr	Gly	Ser	Gly	Ser	Phe	Phe	Arg	
											405					415
gag	gac	aag	gct	ccg	gga	atg	cag	agg	gcc	atc	gac	cag	ctc	gat	gac	1296
Glu	Asp	Lys	Ala	Pro	Gly	Met	Gln	Arg	Ala	Ile	Asp	Gln	Leu	Asp	Asp	
										420			425			430
ctg	agt	ctg	caa	gag	gcc	aga	cg	gg	ctg	tgg	agc	gac	aca	cg	gcc	1344
Leu	Ser	Leu	Gln	Glu	Ala	Arg	Arg	Gly	Leu	Trp	Ser	Asp	Thr	Arg	Ala	
									435			440			445	
gac	atg	gtc	tct	gac	atg	ctg	gtt	cca	ctc	aaa	gtg	gcc	agt	acc	agc	1392
Asp	Met	Val	Ser	Asp	Met	Leu	Val	Pro	Leu	Lys	Val	Ala	Ser	Thr	Ser	
									450			455				460
cac	cga	gtc	cct	gac	tca	ggc	cca	gag	cct	atc	ctg	gcc	tcc	tac	ggc	1440
His	Arg	Val	Pro	Asp	Ser	Gly	Pro	Glu	Pro	Ile	Leu	Ala	Phe	Tyr	Gly	
									465			470				475
agc	cga	ttg	acc	ggc	cgc	cat	aag	gcc	cgc	aag	gcc	cca	gca	ggc	tcc	1488
Ser	Arg	Leu	Thr	Gly	Arg	His	Lys	Ala	Arg	Lys	Ala	Pro	Ala	Gly	Ser	
									485			490				495
aaa	tct	gac	tcc	aac	tcc	agt	aac	ctc	att	cg	ctg	agc	cag	gcc	tca	1536
Lys	Ser	Asp	Ser	Asn	Phe	Ser	Asn	Leu	Ile	Arg	Leu	Ser	Gln	Ala	Ser	
									500			505				510
cct	gag	gat	gcc	ggg	ccc	tgt	cg	ggc	agt	ggc	tgg	gag	gaa	gga	gaa	1584
Pro	Glu	Asp	Ala	Gly	Pro	Cys	Arg	Gly	Ser	Gly	Trp	Glu	Glu	Gly	Glu	
									515			520				525
ggc	cgc	acg	acc	tcc	aca	gag	ccg	tct	gtc	atc	cca	caa	cgg	gaa	gga	1632
Gly	Arg	Thr	Thr	Ser	Thr	Glu	Pro	Ser	Val	Ile	Pro	Gln	Arg	Glu	Gly	
									530			535				540
gat	ggg	cct	ggc	atc	aaa	gac	agg	ccc	atg	gat	gcc	gag	agg	cca	ggc	1680
Asp	Gly	Pro	Gly	Ile	Lys	Asp	Arg	Pro	Met	Asp	Ala	Glu	Arg	Pro	Gly	
					545					550			555			560
cct	gag	ctc	ttt	gat	ccc	agc	agc	tgt	cct	gga	gag	tgg	ctg	agt	gag	1728
Pro	Glu	Leu	Phe	Asp	Pro	Ser	Ser	Cys	Pro	Gly	Glu	Trp	Leu	Ser	Glu	
									565			570				575
cca	gaa	tgg	acc	cta	gag	ggc	atc	cg	gg	tct	cga	gct	caa	ggg	ctc	1776
Pro	Glu	Trp	Thr	Leu	Glu	Gly	Ile	Arg	Gly	Ser	Arg	Ala	Gln	Gly	Leu	
									580			585				590
cca	gct	cac	cat	ccc	cac	ccc	cac	ggg	cca	ccc	agg	acc	acc	agc	ttt	1824
Pro	Ala	His	His	Pro	His	Pro	His	Gly	Pro	Pro	Arg	Thr	Thr	Ser	Phe	
									595			600				605
ctg	cag	cat	gtt	gga	ggg	cac	cac	tga								1851
Leu	Gln	His	Val	Gly	Gly	His	His									
									610			615				

01997001800.ST25

<210> 5
<211> 616
<212> PRT
<213> Mus musculus

<400> 5

Met Ala Thr Ile Gln Ser Glu Thr Asp Cys Tyr Asp Ile Ile Glu Val
1 5 10 15

Leu Gly Lys Gly Thr Phe Gly Glu Val Ala Lys Gly Trp Arg Arg Ser
20 25 30

Thr Gly Glu Met Val Ala Ile Lys Ile Leu Lys Asn Asp Ala Tyr Arg
35 40 45

Ser Arg Ile Ile Lys Asn Glu Leu Lys Leu Leu Arg Cys Val Arg Gly
50 55 60

Leu Asp Pro Asp Glu Ala His Val Ile Arg Phe Leu Glu Phe Phe His
65 70 75 80

Asp Ala Leu Lys Phe Tyr Leu Val Phe Glu Leu Leu Glu Gln Asn Leu
85 90 95

Phe Glu Phe Gln Lys Glu Asn Asn Phe Ala Pro Leu Pro Ala Arg His
100 105 110

Ile Arg Thr Val Thr Leu Gln Val Leu Arg Ala Leu Ala Arg Leu Lys
115 120 125

Glu Leu Ala Ile Ile His Ala Asp Leu Lys Pro Glu Asn Ile Met Leu
130 135 140

Val Asp Gln Thr Arg Cys Pro Phe Arg Val Lys Val Ile Asp Phe Gly
145 150 155 160

Ser Ala Ser Ile Phe Ser Glu Val Arg Tyr Val Lys Glu Pro Tyr Ile
165 170 175

Gln Ser Arg Phe Tyr Arg Ala Pro Glu Ile Leu Leu Gly Leu Pro Phe
180 185 190

Cys Glu Lys Val Asp Val Trp Ser Leu Gly Cys Val Met Ala Glu Leu
195 200 205

His Leu Gly Trp Pro Leu Tyr Pro Gly Asn Asn Glu Tyr Asp Gln Val
210 215 220

01997001800.ST25

Arg Tyr Ile Cys Glu Thr Gln Gly Leu Pro Lys Pro His Leu Leu His
225 230 235 240

Ala Ala Arg Lys Ala His His Phe Phe Lys Arg Asn Pro His Pro Asp
245 250 255

Ala Thr Asn Pro Trp Gln Leu Lys Ser Ser Ala Asp Tyr Leu Ala Glu
260 265 270

Thr Lys Val Arg Pro Leu Glu Arg Arg Lys Tyr Met Leu Lys Ser Leu
275 280 285

Asp Gln Ile Glu Thr Val Asn Gly Gly Gly Ala Val Ser Arg Leu Ser
290 295 300

Phe Pro Asp Arg Glu Ala Leu Ala Glu His Ala Asp Leu Lys Ser Met
305 310 315 320

Val Glu Leu Ile Lys Arg Met Leu Thr Trp Glu Ser His Glu Arg Ile
325 330 335

Ser Pro Ser Ala Ala Leu Arg His Pro Phe Val Ser Met Gln Gln Leu
340 345 350

Arg Ser Ala His Glu Ala Thr Arg Tyr Tyr Gln Leu Ser Leu Arg Gly
355 360 365

Cys Arg Leu Ser Leu Gln Val Asp Gly Lys Pro Pro Pro Pro Val Ile
370 375 380

Ala Ser Ala Glu Asp Gly Pro Pro Tyr Tyr Arg Leu Ala Glu Glu Glu
385 390 395 400

Glu Thr Ala Gly Leu Gly Val Thr Gly Ser Gly Ser Phe Phe Arg
405 410 415

Glu Asp Lys Ala Pro Gly Met Gln Arg Ala Ile Asp Gln Leu Asp Asp
420 425 430

Leu Ser Leu Gln Glu Ala Arg Arg Gly Leu Trp Ser Asp Thr Arg Ala
435 440 445

Asp Met Val Ser Asp Met Leu Val Pro Leu Lys Val Ala Ser Thr Ser
450 455 460

His Arg Val Pro Asp Ser Gly Pro Glu Pro Ile Leu Ala Phe Tyr Gly
465 470 475 480

01997001800.ST25

Ser Arg Leu Thr Gly Arg His Lys Ala Arg Lys Ala Pro Ala Gly Ser
485 490 495

Lys Ser Asp Ser Asn Phe Ser Asn Leu Ile Arg Leu Ser Gln Ala Ser
500 505 510

Pro Glu Asp Ala Gly Pro Cys Arg Gly Ser Gly Trp Glu Glu Gly Glu
515 520 525

Gly Arg Thr Thr Ser Thr Glu Pro Ser Val Ile Pro Gln Arg Glu Gly
530 535 540

Asp Gly Pro Gly Ile Lys Asp Arg Pro Met Asp Ala Glu Arg Pro Gly
545 550 555 560

Pro Glu Leu Phe Asp Pro Ser Ser Cys Pro Gly Glu Trp Leu Ser Glu
565 570 575

Pro Glu Trp Thr Leu Glu Gly Ile Arg Gly Ser Arg Ala Gln Gly Leu
580 585 590

Pro Ala His His Pro His Pro His Gly Pro Pro Arg Thr Thr Ser Phe
595 600 605

Leu Gln His Val Gly Gly His His
610 615

<210> 6
<211> 11351
<212> DNA
<213> Mus musculus

<400> 6
ttcttccctt ctgatttctc accaaaatgt caagcttctt cttatTTTat ttttattctt 60
tatttattgg ttttcaaga gagggctttt cagccttggaa tgtcctggaa ctcagtagac 120
ccgactggcc ttgaactcac agagatctac ctgcattcccc ctccggagtg ctgggattaa 180
gagcatgtgc cacaactgcc tggcaagcag cctcatcttcc tatggttcc atacttcaga 240
gctgacagat ctccattcct ggggggtggg gggaggagct tctggggatg cctccataca 300
ccatatacgc catatacacc atatatacca tatacatcat atataccata taaaacatata 360
acaccatata ctggagctgt gggatggca gttccatcc tgtctctggc tcccaaattga 420
ctgacttaag cataagtgtct ctaaaaaact ttttgttccc tgcttaggcag tgcttgtgct 480
ctccttaat cccagcactc tttaattcca gcagtttagga ggcggaggca aggcagatct 540
ctgtgagttc gaggccagcc tgcattcacag agttccaaga gagccaaggc tacacagaga 600

01997001800.ST25

aaccttgtct	gggggggggg	ggggAACCAA	aagagcattt	attgtttttt	cagaggatct	660
gggttggatt	cccagagccc	accttgaagc	tcacaaccat	ctgtaactct	agtcacagcg	720
gatatatata	tatatatattt	tatagcctgg	gaatgggca	gtaagcggga	tgtgaagtga	780
ataattaatt	aattaattag	ggggctggag	agatgactca	gcaggtaaag	gcagtggctg	840
ctcttccaca	ggtcctgagt	tcaattccca	gcaaccacat	ggtggctcac	aaccatctgt	900
aatgggattc	tatgcccttt	tctggtgtgt	ctgaagacag	ctgacatgca	gtcatataaa	960
tagaataaat	aatctaaaaa	aaaaacccaa	aacaaaacca	tatattaaat	agaaaaacgt	1020
atggaagaga	aaaaacaaga	caaggagaaa	tgcctttgt	ttaacatcca	tttcctgaac	1080
ctaacttcag	tgtcttctcc	cagctattgt	cccttgcctca	tgtcaccttc	tcagggactg	1140
tcctacacct	tgtcgtagat	ggtttcttcc	ctccctgatc	ttctcaggac	ctcagcctac	1200
cctcttgccct	tatggaggg	ctcacccagt	cagggcctga	accctcacc	agcctcatct	1260
gcctgggtcc	tgccttagcc	tcctgctgg	ggtctggagc	ctccatcctt	gccttctaca	1320
gtttgccttt	cttcatgtct	gactgagtgg	tcgttccctt	acctgaagcc	ctcatggctc	1380
cccagtgtct	ggttcaaacg	tttttagcct	gcattcagt	ccttcacaa	cctggatctt	1440
actttatcta	cataccccc	ccatgcttca	cacacacaca	cccacacaca	cacacacaca	1500
cacacacaca	cacagactct	ctaactttct	tcactctcat	atgcctgtag	gtatgtccca	1560
cttctgaact	cccaaggtca	accattaaaa	tctcactcag	tccaccctgt	ccgtgcttct	1620
ccaggattcc	ggtcagcggg	tggggaggg	gtcccagcct	ggtacccac	cccctccatt	1680
ccagcctggg	actcaggtct	ctaacaacag	aatcaaagcc	acttagcaac	gctgaaaccc	1740
attcaggggg	gcctgagccc	cctcatccca	agccaagagg	gctttggggg	aggggtgcag	1800
cccctggtag	actcaactgt	tggccaaggg	ggtcaagggg	cgtcagggag	acaggggctg	1860
aactcatata	aggagagaca	cgagtgttgt	tatcttcccc	ctgctaggag	gactagctag	1920
ggccatcat	cagggtggga	ggtctaggca	accaagccag	ttgttgtaaa	ggcagagtag	1980
tgactggcag	ccaaggtacc	atggccacca	tccagtcaga	gactgactgc	tacgacatca	2040
ttgaagttct	ggcaagggc	actttggag	aggtggccaa	gggctggcgt	cgagtgatcg	2100
gtgaatggt	ggccatcaag	atccgtaaaga	acgatgcgt	ccgaagccgc	atcatcaaga	2160
atgagctgaa	gctgctgcgc	tgcgtgcgt	gcctggaccc	tgacgaggcc	cacgttatcc	2220
gcttccttga	gttctccac	gatcccctca	agttctacct	ggtcttcgag	cttttggagc	2280
aaaacctctt	tgagttccag	aaagagaaca	acttcgcacc	ctttcctgcc	aggcacatcc	2340
gcacggtcac	actgcaggt	ctaagagcgc	tggcccggt	caaggaactg	gccatcatcc	2400
acgctgacct	caagcctgaa	aacattatgt	tggttagacca	gaccggctgc	cccttcaggg	2460

01997001800.ST25

tcaaggtag	tgaggctgcc	tggaaatgg	cttgcttag	ttcttgatg	ctctgcta	2520
acatgggtct	ccctagtcag	ttccgtgacg	cagctccggg	tgtccctgaa	ccccaaagctg	2580
ccccctcttgc	ctgctctctg	gctgtcttct	gtatcccatc	ccaattcttgc	ctttgttttgc	2640
ttttgttttc	gagacagagt	cgatgtggca	caggctggcc	ttgaactcac	tgtgtagctg	2700
aggacgactt	gaactcatgg	cctatctgcc	ctccctgcct	ccacgaccta	agtgcgtatgt	2760
gtcacctaag	tcaccacagc	cagctcgctt	tgttgtgttt	tgttttttga	agacaggatc	2820
tcagggagtc	caggctggtc	tggaatttga	gtgggtttcc	cttctcaagt	accgggattt	2880
caggcattca	ccatcttacc	tggcttctcc	atctcaactc	tgaggtcctt	tctatcgaag	2940
actggaggtc	ttctgtgcct	ccccctctagg	tcctgagtc	gcccaaccct	gcccgttgg	3000
cttacttctt	ctggctcagg	tctgggcctc	gtgggtctgg	cattctagtg	ggggagatgg	3060
tagcagggta	agaagtaaag	cgtgttgtgg	atgtgagacc	agagaaaaca	ggagagagag	3120
gctgggaact	gctcagacat	gggaagtgg	agacagggag	gtcacacttc	aggaggtctt	3180
gaggggaaga	gaaggccatg	gagaaggat	gagttccag	gatgaaggag	gagccagcac	3240
aaaggctcga	ggttaggagca	tgtctaagta	ttctagcaac	acacagggga	gttctgtgca	3300
gttgaagcac	aatatgtgg	gagcaaagag	ggagaaaagg	acaccaagga	ggttaggggt	3360
gggttgcaca	aatcctcata	ggcacagtca	agattggttt	tgttttggta	tgtatatctc	3420
cctccatgg	ttcacaatgt	atccctggct	ggccttgaac	ttactatgt	gacgaggcag	3480
gcttcaaact	catggcagat	cctctgcct	ctgcctccca	aacaatggac	tcaaagttac	3540
acaccaacac	gctaggcttg	cagacgatt	cagagcagca	ggatggctc	tgacttaggg	3600
gctcatcttgc	gggggaagta	ggaccaagaa	agcagatggg	gtgatccaag	aggagtccca	3660
ggtaaaagat	gtaactgggg	cattcgtgga	ttccgggcag	attttagagc	tagagacaac	3720
agaatttagaa	ttgattgatg	ggtttcacag	tgtgagggag	aggggctggg	gagatgctca	3780
gatagtaatg	tccccgctga	acaagcatgg	aaacctcagt	gcagaccctt	accatcccc	3840
tgaaaagacg	gctgtggcag	cacacctgta	atatcgtgt	aggggaggt	gagacaggag	3900
gattcctaga	gcttgatggc	cagccagtct	agccaatcag	caggctcggg	gttccaggag	3960
gggagggatc	ttatctcata	tataaaagtt	agagagcgt	agaagacatg	cgatgcatgt	4020
gtgatgacac	acatgtgcac	acgcatacaa	acatctacac	atacatttg	aaaaagaagg	4080
gccagcaaga	tggctcagcc	agttcaggtg	cttgctgcca	agcctaagga	cttgagtc	4140
gtagccagaa	cccatatgg	gggagcagag	aactgacttc	ctgactctgg	aagttgtcct	4200
ctgacctcta	cacatatacc	actgcatttgc	catatccctc	ccccactaa	attcagtttgc	4260
aaaatgaaaa	agtgtgaggg	gcagctggc	attgtggcag	cctcctata	ttccagcact	4320
gcacaagtgg	aggcaggagg	attaaaaatt	caaggtcatc	cttggctgtt	aaacaagttc	4380

01997001800.ST25

aaggtcagct tgcactttca aggtctgtct tgcactacct gagacctcat cttaaagaa	4440
aagatgtgag agaggctgag tgggctcaag ttgagccaga gcctgcggat ctagacaaat	4500
gcaagggtgg tctagcctct gttcctgttc ctgaccctgg gtgggcacct aagctgtccc	4560
ttgttcccc tagatccac ttctgctgag cctctgtctg ggcctcatca acctactcag	4620
acacccctct tgtgcctcct ccatcagagc tcagactcct ctgcctgctt atctgtcagc	4680
aaggcactgg tcatgactgg gctggcagca gcacccaagg gcagggctgg accaaagctg	4740
cctatactgt gcctctcccc gtgccccact gaatgttaga gacacagaga caggaagaga	4800
tgggtatttc tgccctgttg gatggaagga cagtgagccg agaggaagag agctctgtag	4860
acctaacagg gctcacacag cacctgggg tcgctggcac ccttcaagtg cttcagaat	4920
gaagggactc cacatacact ggctcaactc tcagtgtcac tgaagtccctt gggggcgttg	4980
agtccagact aataactatt tcatgattgg ctttgtgtgc atggaggtaa gaggtgacta	5040
aatggataaa taaatgaata aataaacgca gggaaagctgc agcctgcctt gagtcacagg	5100
aattcacagt gagactggaa gagcgccacc tggtggcgag agggaaaggca ggccgcctacc	5160
catggcccat ggattaccaa gaagcttggt aattacaagc tgaaggcctt cgggggtgttgc	5220
tcagtgtctg acggtaaaga tcttagagga cttggttta ggatggtacc tttccagtc	5280
atgacacaga aacaaagaca gagacactgg gagatgagga ttagctgaag aggcaatggg	5340
agagagagag agaaagagag agagagagac agagccactg ggtggggca gcacatgctt	5400
ttaatatcag cacttgggag gtacaggtag aggtggattt ctgagttcta ggccatcctg	5460
gtctacagag tgagtttaag gaccaccagg gttacacaga gaaaccctgt cttaaaaaac	5520
aaatacacac acatacacac acacacacac atacatatac atacatataat atatgagaag	5580
ggagccagac ctggtaaaac atgcctataa tcccagatta ttgtaccttc tacatttcct	5640
ctcttatgaa tgaccctgcc tgaagttcaa tctctaggac catgaaagac agacacacaa	5700
atcaaaggga ggacaatact gattgggttaaaatgcctac tagttccagg cctccagaga	5760
cacagccctg aataaaatac aaagcttttgc ttgtcatggg actggagttc tatttttttt	5820
ttcatttttattt atgtgagtgc aaatgtatgg atgtatggtgc ttccaagagg	5880
tcagaggcgt ttggattccc cctggacta gagttccaga caggtgtgag ctgccatgtg	5940
ggtgctggga gccaaacctg gattccctgc aagagcagcc agtgcctttt accactgagc	6000
catctctcag gccttagcggg ttaagtgcctt gctgcacaca agcagaagag cctaaattca	6060
gatccccagg gacccataa aagctggct tgactttata atcccaggc tgagggatg	6120
taagggaaaga caagaagatc ctgagggctc agtggcccg ctatcttgcc aaagttgtga	6180
gtttcaggtt cactaagaga cttgcctca caaaataagg ttacagcggt agaggaagat	6240

01997001800.ST25
agaggacctt tggccttata catgcacaca tgggtatga caccacata tgcctataac 6300
acctccaaca cacacaacac cccccctcag ggaaatatat atatagtatg tgaaatgatg 6360
ttaaaatcat agctgggagc tgggtgaaag aacaggaatt caaggacatc cttggctaca 6420
taaccaggtt gaagccagcc tggctatat gagaccctgt ctcaaaacta accaacaaaa 6480
aggacagagg atatgggtga atactgcct actatgcact acagcagggg gagggtccc 6540
actattatag gcacaagttc aagcagagaa tcagacagag ccagacctga cacctgacac 6600
agaagcaata gctagaggac agaggcaggg tcattcataa gaaaggaagt gtagaaggt 6660
caagagctag gcagacacag gagatacaca gggatgagtc ccaggagggg cctatcctgt 6720
catctctacc actccaccaa cccagctgcc ctgtgctcca tcccctctgt cctccatagg 6780
tgatcgactt tggctcgcc agcatattca gtgaggtacg ctatgtaaag gaggcttaca 6840
tccagtcggc cttctacagg gccccagaga tcctgctgg gctgcccttc tgtgagaagg 6900
tggacgtgtg gtctctggc tggcatgg ccgagctaca tctggctgg cctctctacc 6960
caggcaacaa ttagtatgac caggtgcgt acatctgtga gacccagggc ttacccaagc 7020
cccatggct gcatgcggc cgcaaggctc accacttctt caagcgtaac ccccaccc 7080
atgccaccaa cccctggcag ctgaagtccct ctgctgacta cctagctgag accaaggat 7140
gggggagcat gcagggtgaa gacagcctgt gctgggggt ggggacgata ctatatcgcc 7200
atgtctcttt ggctggactg agggcttagg tggaaatgtgg agcctgagtt aggtcacata 7260
tcctccctgt agcagtggga gagtgatgga ttggaaatca agaatctgtt atgaggggaa 7320
cgactggaga attgaaatag caagagaact tccagtcata tcatggcag aagtcagggg 7380
gtgatttga gtctagatac atggcaggct ggtgtcccc accccccacc aggtacgtcc 7440
tctggagcgc cgcaagtaca tgctcaaattc cttggaccag attgagacag tgaatggtgg 7500
tggagctgtg agccggctga gtttccaga cccggaggcc ctggcggAAC acgcagacct 7560
caagagcatg gtggagctga tcaaacgcatt gctgacatgg gagtcgcacg aacgcattcag 7620
tcccagtgcg gcccgcgtc acccctcgt gtccatgcag cagctgcgg a gtggccacga 7680
ggccacccgc tactaccagc tgctgcgtcagg ctgtccctgc aggtggatgg 7740
caagccaccc ccacctgtca tagccagcgc agaggacggg cctccctact accgcctggc 7800
tgaggaggag gagactgcag gcctgggtgg tggacaggc agtgggtcct tttcaggga 7860
ggacaaggct ccggaaatgc agagggccat cgaccagctc gatgacactga gtctgcaaga 7920
ggccagacgg gggctgtgga ggcacacacg ggccgacatg gtctctgaca tgctgggtcc 7980
actcaaagtg gccagttacca gccaccgagt ccctgactca ggcccagagc ctatcctggc 8040
cttctacggc agccgattga ccggccgcca taaggcccgc aaggccccag caggctccaa 8100
atctgactcc aacttcagta acctcattcg gctgagccag gcctcacctg aggtgcgg 8160

01997001800.ST25

gccctgtcgg ggcagtggct	gggaggaagg agaaggccgc	acgacacctca	cagagccgtc	8220			
tgtcatccca	caacgggaag gagatgggcc	tggcatcaa	gacaggccca	tggatgccga	8280		
ggtaagtggg	gtgcagactg gcacccagag	cttaattgac	ggtgcacagg	tgacagggcc	8340		
gtgcttctta	cagctgcagc atctgtcatc	tcaacacggg	cccaagattc	agtaaatact	8400		
gacccctgc	acaagggtggc agggctcagc	tcacaccaat	accctcagga	ctggacaagg	8460		
ctgatacaa	ctctaattaa ggatggcaca	gaaaacaggc	acctagtat	gggctggta	8520		
agaaatgggt	gaggtgctgg gtgggtgg	acattatctg	taatcccggg	gagctcaa	8580		
aggagggtca	tctcaagg	tc aagtctagtt	tgggtcataa	caagacccta	tctcaaaaag	8640	
caaacagtaa	tattccctcc	ctacaaaag ggctacagat	ttagttgtgc	agtagagttc	8700		
ttgcctagta	tctaccagtg	agagaatggg	gactctccta	cacagagtgc	ttaccaatgt	8760	
gaggggctgg	gggtgtggct	cagtggtaga	gcccctgcct	agaatccctc	agtgagggac	8820	
tggggcattg	gctcagtgg	agagccctg	cctagaatcc	cccagtgagg	ggctggggc	8880	
gtggctcagt	ggttagagccc	ctgcctagaa	tccccagtg	aggggctggg	gggtgtggctc	8940	
agtggtagag	cccctgccta	gaatccccca	gtgagggc	ggggacgtgg	tccagaggca	9000	
gagcatttgc	ctggctgtcc	aaggcttca	tccctaatac	ctttgcaatg	tggaaaggcc	9060	
tacacaggg	gtgagggc	tcatacctgc	tcactcc	cagttagacag	gtacacac	9120	
cagcaggtac	ccataattct	tgctgatatt	ctttctttt	ccccccaca	gaggccaggc	9180	
cctgagctct	ttgatcccag	cagctgcct	ggagagtggc	tgagtgagcc	agaatggacc	9240	
ctagagggca	tccggggc	tcgagctcaa	gggctcccag	ctcaccatcc	ccaccccccac	9300	
ggccaccca	ggaccaccag	ctttctgcag	catgttggag	ggcaccactg	atggggactc	9360	
acccctatcg	tttcatgggg	tctgagctag	ctggctggc	gttccc	ttgatccgaa	9420	
atggcacctt	agagccatcc	tctgaaccta	cagattattc	ttacagaaaa	atagaaatcc	9480	
agatttcctt	attccctgc	ccctggcaca	tgcctgtatc	ccaccctaaa	tgttggaggt	9540	
cgtcagggc	tggctgagg	ccctggc	agttagttgg	gaagaggctg	caccctgg	9600	
gccatgactg	tgcctggcc	tgcctgc	tgtgtat	aataaataac	tgttccaaac	9660	
cctgctcctg	cctgttacca	ctgggtgaac	ctgttaccacc	catattggc	caagggggca	9720	
cccagggc	gcctgc	cc	tgctgtact	gttggccac	tggctgaacc	9780	
gtcagtggca	ggaaaaagct	gcgcagg	cagtaac	tgctctat	acactaaatt	9840	
aaacctggta	tggggcagtg	ggttgtaat	tctaagact	caggagactg	aggcaggaga	9900	
attacaaggt	caagaccagt	ttgggctt	at	gatgagac	tgtcaacaca	ggggtttag	9960
gggagatggg	atgaggcaag	ggcctggc	cttggaaatc	tacccttagg	atgttca	cat	10020

01997001800.ST25

gttggacaag gaccctggc ttcgtcctct atgtctgtga tggacaggcc atgcgctcgc 10080
tcgctcatgc tctggacatg ttaagtgtaa acacactggt aggaataaat tcagacttcg 10140
cacatgctgt gttgttcaca tacgcacatg ctccgggttt cagatatgtt agtccagctg 10200
ccacttgggc ccggccttat tccccccac ccccacccac acccaccac ctcccattcc 10260
catcccaac ggccgtaaat ggcattcagc agtggttcta cccgcactgc tctgtggagc 10320
atactcgta caaacatgct ggttctacgc atgctcagcc catgcttgcc agtgcggtca 10380
cacactgcat gcccagccca cgccagcctt cgtgcgcact gcatgctgtc accagcagaa 10440
gtccataccc cctcccccct aacaaacata ccatctcata ccactcagtt aagcacagggc 10500
tatacagaca attatttact tataatcttgc gccccttggg ggtgggccaa aggtctggc 10560
ccagcatgca cccccacttc tttggggccc aatccccagc tctgcttaggt ccacaggggc 10620
cagagtgtca ggccagtggc ggtggaggta gcagcaggag tatagtggag agtacagagc 10680
cacacgggat agacagagggc aaggcatgg ggacagtaac caggacccag agctgagtcc 10740
aaggaggcct ggaaggctt gacctgtccg tcgggctgag cctcaaagca ggcggcaggc 10800
attgcccaca ctgttggctg aggtgtcgag atcgtggctg tatggggatt cccagtctct 10860
caggaaaaca gcctccagct gactgcgcaa gccaccatgc ccgttctgtc tcaccagcag 10920
ggaggtgcct gctgtctccg tgaagtagct tccagaccag ttggaggttc ctggagcaa 10980
ggggtggagt gagggtctga tgggtggcca gaccctagtg cccaggcctt tcctttgata 11040
tggtactggg ggcacttacc aatgtatgag gcacgttcag tcaccatgta cttgttgtgg 11100
ttgacacggg cataggggat tcgggcctgg gactcatccg tagggaccac aaacagttc 11160
tgcaggggag aggaggatgg tgaggtgggg gctcaagggtg caggtgggggt gtctctgaga 11220
agtccctggga tggtaggatg gcatgtgaat ggtatctcca aaaggcactt ggctgcttct 11280
ctgggaaggg tggatcctgg gacaaaata ggtcccaggg cagctgggcc tcggtaaca 11340
cgagctgagg c 11351

<210> 7

<211> 1851

<212> DNA

<213> *Macaca fascicularis*

<220>

<221> CDS

<222> (1)..(1848)

<400> 7

atg gct acc acc cag tca gag acc gac tgc tac gac atc atc gag gtc
Met Ala Thr Thr Gln Ser Glu Thr Asp Cys Tyr Asp Ile Ile Glu Val
1 5 10 15

48

ttg ggc aag ggg acc ttc ggg gag gta gcc aag ggc tgg cgg cgg agc

96

01997001800_ST25

Leu	Gly	Lys	Gly	Thr	Phe	Gly	Glu	Val	Ala	Lys	Gly	Trp	Arg	Arg	Ser	
20					25						30					
acg	ggc	gag	atg	gtg	gcc	atc	aag	atc	ctc	aag	aac	gac	gcc	tac	cgc	144
Thr	Gly	Glu	Met	Val	Ala	Ile	Lys	Ile	Leu	Lys	Asn	Asp	Ala	Tyr	Arg	
35					40						45					
aac	cgc	atc	atc	aag	aat	gag	ctg	aag	ctg	ctg	cac	tgc	atg	cga	gac	192
Asn	Arg	Ile	Ile	Lys	Asn	Glu	Leu	Lys	Leu	Leu	His	Cys	Met	Arg	Gly	
50					55					60						
ctg	gac	cct	gag	gag	gcc	cac	gtc	atc	cgc	ttc	ctc	gag	ttc	ttc	cac	240
Leu	Asp	Pro	Glu	Glu	Ala	His	Val	Ile	Arg	Phe	Leu	Glu	Phe	Phe	His	
65					70				75				80			
gac	gcc	ctc	aag	ttc	tac	ctg	gtc	ttc	gag	ctg	ctg	gag	caa	aac	ctt	288
Asp	Ala	Leu	Lys	Phe	Tyr	Leu	Val	Phe	Glu	Leu	Leu	Glu	Gln	Asn	Leu	
85					90							95				
ttt	gag	ttc	cag	aag	gag	aac	aac	ttc	gct	ccc	ctc	cct	gcc	cgc	cac	336
Phe	Glu	Phe	Gln	Lys	Glu	Asn	Asn	Phe	Ala	Pro	Leu	Pro	Ala	Arg	His	
100					105							110				
atc	cgt	aca	gtc	acc	ctg	cag	gtg	ctc	aga	gcc	ctg	gcc	cgg	ctc	aag	384
Ile	Arg	Thr	Val	Thr	Leu	Gln	Val	Leu	Arg	Ala	Leu	Ala	Arg	Leu	Lys	
115					120					125						
gag	ctg	gca	atc	atc	cac	gct	gat	ctc	aag	cct	gag	aat	atc	atg	ctg	432
Glu	Leu	Ala	Ile	Ile	His	Ala	Asp	Leu	Lys	Pro	Glu	Asn	Ile	Met	Leu	
130					135				140							
gtg	gac	cag	acc	cgc	tgc	ccc	ttc	agg	gtc	aag	gtg	att	gac	ttc	ggc	480
Val	Asp	Gln	Thr	Arg	Cys	Pro	Phe	Arg	Val	Lys	Val	Ile	Asp	Phe	Gly	
145					150				155				160			
tct	gcc	agc	att	ttc	agc	gag	gtg	cgc	tac	gtg	aag	gag	cca	tac	atc	528
Ser	Ala	Ser	Ile	Phe	Ser	Glu	Val	Arg	Tyr	Val	Lys	Glu	Pro	Tyr	Ile	
165					170					175						
cag	tcg	cgc	ttc	tac	cgg	gcc	ccc	gag	atc	ctg	ctg	ggg	ctg	ccc	ttc	576
Gln	Ser	Arg	Phe	Tyr	Arg	Ala	Pro	Glu	Ile	Leu	Leu	Gly	Leu	Pro	Phe	
180					185					190						
tgc	gag	aag	gtg	gac	gtg	tgg	tcc	ctg	ggc	tgt	gtc	atg	gct	gag	ctg	624
Cys	Glu	Lys	Val	Asp	Val	Trp	Ser	Leu	Gly	Cys	Val	Met	Ala	Glu	Leu	
195					200					205						
cac	ctg	ggc	tgg	ccc	ctc	tac	ccc	ggc	aat	aac	gag	tac	gac	cag	gtg	672
His	Leu	Gly	Trp	Pro	Leu	Tyr	Pro	Gly	Asn	Asn	Glu	Tyr	Asp	Gln	Val	
210					215					220						
cgc	tac	atc	tgc	gaa	acc	cag	ggc	ctc	ccc	aag	ccg	cac	ctg	ctg	cac	720
Arg	Tyr	Ile	Cys	Glu	Thr	Gln	Gly	Leu	Pro	Lys	Pro	His	Leu	Leu	His	
225					230					235				240		
gcc	gcc	cgc	aag	gcc	cac	cac	ttc	ttt	aag	cgc	aac	ccc	cac	cct	gac	768
Ala	Ala	Arg	Lys	Ala	His	His	Phe	Phe	Lys	Arg	Asn	Pro	His	Pro	Asp	
245					250					255						
gcc	gcc	aac	ccc	tgg	cag	ctc	aag	tcc	tcg	gct	gac	tac	ctg	gcc	gag	816
Ala	Ala	Asn	Pro	Trp	Gln	Leu	Lys	Ser	Ser	Ala	Asp	Tyr	Leu	Ala	Glu	
260					265					270						

01997001800.ST25																
acg	aag	gtg	cgc	cca	ctg	gag	cgc	cgc	aag	tat	atg	ctt	aag	tcc	ttg	864
Thr	Lys	Val	Arg	Pro	Leu	Glu	Arg	Arg	Lys	Tyr	Met	Leu	Lys	Ser	Leu	
275		280							285							
gac	cag	atc	gag	aca	gtg	aat	ggt	ggc	agt	gtg	gcc	agt	cgg	ctg	acc	912
Asp	Gln	Ile	Glu	Thr	Val	Asn	Gly	Gly	Ser	Val	Ala	Ser	Arg	Leu	Thr	
290		295							300							
ttc	ccc	gac	cgg	gag	gca	ctg	gca	gag	cac	gcc	gac	ctc	aag	agc	atg	960
Phe	Pro	Asp	Arg	Glu	Ala	Leu	Ala	Glu	His	Ala	Asp	Leu	Lys	Ser	Met	
305		310							315						320	
gtg	gag	ctg	atc	aaa	cgc	atg	ctg	acc	tgg	gaa	tca	cat	gaa	cgc	atc	1008
Val	Glu	Leu	Ile	Lys	Arg	Met	Leu	Thr	Trp	Glu	Ser	His	Glu	Arg	Ile	
									330						335	
agc	ccc	agt	gct	gcc	ctg	cgc	cac	ccc	ttc	gtg	tcc	atg	cag	cag	ctg	1056
Ser	Pro	Ser	Ala	Ala	Leu	Arg	His	Pro	Phe	Val	Ser	Met	Gln	Gln	Leu	
									345						350	
cgc	aat	gcc	cac	gag	acc	acc	cac	tac	tac	cag	ctc	tcg	ctg	cgc	agc	1104
Arg	Asn	Ala	His	Glu	Thr	Thr	His	Tyr	Tyr	Gln	Leu	Ser	Leu	Arg	Ser	
									360						365	
tac	cgc	ctc	tcg	ctg	cag	gtg	gag	ggc	aag	ccc	ccc	gcg	cct	gtc	gtg	1152
Tyr	Arg	Leu	Ser	Leu	Gln	Val	Glu	Gly	Lys	Pro	Pro	Ala	Pro	Val	Val	
						370	375									
gct	gca	gaa	gat	ggg	acc	ccc	tac	tac	cgt	ctg	gct	gag	gag	aag	gag	1200
Ala	Ala	Glu	Asp	Gly	Thr	Pro	Tyr	Tyr	Arg	Leu	Ala	Glu	Glu	Lys	Glu	
						385	390								400	
gct	gcg	ggc	atg	ggc	agt	gtg	gcc	agc	agc	agc	ccc	ttc	ttc	cga	gag	1248
Ala	Ala	Gly	Met	Gly	Ser	Val	Ala	Ser	Ser	Ser	Pro	Phe	Phe	Arg	Glu	
						405			410						415	
gag	aag	gca	cca	ggt	atg	caa	aga	gcc	atc	gac	cag	ctg	gac	gac	ctg	1296
Glu	Lys	Ala	Pro	Gly	Met	Gln	Arg	Ala	Ile	Asp	Gln	Leu	Asp	Asp	Leu	
						420			425						430	
agt	ctg	cag	gag	gct	ggg	cat	ggg	ctg	tgg	ggt	gag	acc	tgc	acc	gat	1344
Ser	Leu	Gln	Glu	Ala	Gly	His	Gly	Leu	Trp	Gly	Glu	Thr	Cys	Thr	Asp	
						435	440								445	
gtg	gtc	tcc	gac	atg	atg	gcc	ccc	ctc	aag	gca	gcc	atc	act	ggc	cgc	1392
Val	Val	Ser	Asp	Met	Met	Ala	Pro	Leu	Lys	Ala	Ala	Ile	Thr	Gly	Arg	
						450	455								460	
cac	atg	ccc	gac	tca	ggc	ccc	gag	ccc	atc	ctg	gcc	ttc	tat	agc	agc	1440
His	Met	Pro	Asp	Ser	Gly	Pro	Glu	Pro	Ile	Leu	Ala	Phe	Tyr	Ser	Ser	
						465	470								480	
cgc	ctg	gca	ggc	cgc	cac	aag	gcc	cgc	aag	cca	cct	gcg	ggt	tcc	aaa	1488
Arg	Leu	Ala	Gly	Arg	His	Lys	Ala	Arg	Lys	Pro	Pro	Ala	Gly	Ser	Lys	
						485			490						495	
tcc	gac	tcc	aac	ctc	agc	aac	ctc	atc	cg	ctg	agc	cag	gtc	tcg	cct	1536
Ser	Asp	Ser	Asn	Leu	Ser	Asn	Leu	Ile	Arg	Leu	Ser	Gln	Val	Ser	Pro	
								500		505					510	
gag	gat	gac	agg	ccc	tgc	cg	ggc	agc	agc	tgg	gag	gaa	gga	gag	cat	1584
Glu	Asp	Asp	Arg	Pro	Cys	Arg	Gly	Ser	Ser	Trp	Glu	Glu	Gly	Glu	His	
						515			520						525	

01997001800.ST25

ctc ggg gcc tct gct gag cca ccg gcc atc ctg cag cga gat ggg gat	1632
Leu Gly Ala Ser Ala Glu Pro Pro Ala Ile Leu Gln Arg Asp Gly Asp	
530 535 540	
ggg ccc aac att gac aac atg acc atg gag gct gag agg cca gac cct	1680
Gly Pro Asn Ile Asp Asn Met Thr Met Glu Ala Glu Arg Pro Asp Pro	
545 550 555 560	
gag ctc ttc gac ccc agc agc tgt ccc gga gaa tgg ctg agt gag cca	1728
Glu Leu Phe Asp Pro Ser Ser Cys Pro Gly Glu Trp Leu Ser Glu Pro	
565 570 575	
gac tgg acc ctg gag ggc gtc agg ggc cca cgg gct cag ggg ctc cca	1776
Asp Trp Thr Leu Glu Gly Val Arg Gly Pro Arg Ala Gln Gly Leu Pro	
580 585 590	
ccc cgc cgc tcc cac cag cat ggt ccg ccc cgg ggg gcc acc agt ttc	1824
Pro Arg Arg Ser His Gln His Gly Pro Pro Arg Gly Ala Thr Ser Phe	
595 600 605	
ctc cag cat gtc acc ggg cac cac tga	1851
Leu Gln His Val Thr Gly His His	
610 615	

<210> 8
 <211> 616
 <212> PRT
 <213> Macaca fascicularis
 <400> 8

Met Ala Thr Thr Gln Ser Glu Thr Asp Cys Tyr Asp Ile Ile Glu Val
 1 5 10 15

Leu Gly Lys Gly Thr Phe Gly Glu Val Ala Lys Gly Trp Arg Arg Ser
 20 25 30

Thr Gly Glu Met Val Ala Ile Lys Ile Leu Lys Asn Asp Ala Tyr Arg
 35 40 45

Asn Arg Ile Ile Lys Asn Glu Leu Lys Leu Leu His Cys Met Arg Gly
 50 55 60

Leu Asp Pro Glu Glu Ala His Val Ile Arg Phe Leu Glu Phe Phe His
 65 70 75 80

Asp Ala Leu Lys Phe Tyr Leu Val Phe Glu Leu Leu Glu Gln Asn Leu
 85 90 95

Phe Glu Phe Gln Lys Glu Asn Asn Phe Ala Pro Leu Pro Ala Arg His
 100 105 110

Ile Arg Thr Val Thr Leu Gln Val Leu Arg Ala Leu Ala Arg Leu Lys
 115 120 125

01997001800.ST25

Glu Leu Ala Ile Ile His Ala Asp Leu Lys Pro Glu Asn Ile Met Leu
130 135 140

Val Asp Gln Thr Arg Cys Pro Phe Arg Val Lys Val Ile Asp Phe Gly
145 150 155 160

Ser Ala Ser Ile Phe Ser Glu Val Arg Tyr Val Lys Glu Pro Tyr Ile
165 170 175

Gln Ser Arg Phe Tyr Arg Ala Pro Glu Ile Leu Leu Gly Leu Pro Phe
180 185 190

Cys Glu Lys Val Asp Val Trp Ser Leu Gly Cys Val Met Ala Glu Leu
195 200 205

His Leu Gly Trp Pro Leu Tyr Pro Gly Asn Asn Glu Tyr Asp Gln Val
210 215 220

Arg Tyr Ile Cys Glu Thr Gln Gly Leu Pro Lys Pro His Leu Leu His
225 230 235 240

Ala Ala Arg Lys Ala His His Phe Phe Lys Arg Asn Pro His Pro Asp
245 250 255

Ala Ala Asn Pro Trp Gln Leu Lys Ser Ser Ala Asp Tyr Leu Ala Glu
260 265 270

Thr Lys Val Arg Pro Leu Glu Arg Arg Lys Tyr Met Leu Lys Ser Leu
275 280 285

Asp Gln Ile Glu Thr Val Asn Gly Gly Ser Val Ala Ser Arg Leu Thr
290 295 300

Phe Pro Asp Arg Glu Ala Leu Ala Glu His Ala Asp Leu Lys Ser Met
305 310 315 320

Val Glu Leu Ile Lys Arg Met Leu Thr Trp Glu Ser His Glu Arg Ile
325 330 335

Ser Pro Ser Ala Ala Leu Arg His Pro Phe Val Ser Met Gln Gln Leu
340 345 350

Arg Asn Ala His Glu Thr Thr His Tyr Tyr Gln Leu Ser Leu Arg Ser
355 360 365

Tyr Arg Leu Ser Leu Gln Val Glu Gly Lys Pro Pro Ala Pro Val Val

01997001800_ST25

370

375

380

Ala Ala Glu Asp Gly Thr Pro Tyr Tyr Arg Leu Ala Glu Glu Lys Glu
385 390 395 400

Ala Ala Gly Met Gly Ser Val Ala Ser Ser Ser Pro Phe Phe Arg Glu
405 410 415

Glu Lys Ala Pro Gly Met Gln Arg Ala Ile Asp Gln Leu Asp Asp Leu
420 425 430

Ser Leu Gln Glu Ala Gly His Gly Leu Trp Gly Glu Thr Cys Thr Asp
435 440 445

Val Val Ser Asp Met Met Ala Pro Leu Lys Ala Ala Ile Thr Gly Arg
450 455 460

His Met Pro Asp Ser Gly Pro Glu Pro Ile Leu Ala Phe Tyr Ser Ser
465 470 475 480

Arg Leu Ala Gly Arg His Lys Ala Arg Lys Pro Pro Ala Gly Ser Lys
485 490 495

Ser Asp Ser Asn Leu Ser Asn Leu Ile Arg Leu Ser Gln Val Ser Pro
500 505 510

Glu Asp Asp Arg Pro Cys Arg Gly Ser Ser Trp Glu Glu Gly Glu His
515 520 525

Leu Gly Ala Ser Ala Glu Pro Pro Ala Ile Leu Gln Arg Asp Gly Asp
530 535 540

Gly Pro Asn Ile Asp Asn Met Thr Met Glu Ala Glu Arg Pro Asp Pro
545 550 555 560

Glu Leu Phe Asp Pro Ser Ser Cys Pro Gly Glu Trp Leu Ser Glu Pro
565 570 575

Asp Trp Thr Leu Glu Gly Val Arg Gly Pro Arg Ala Gln Gly Leu Pro
580 585 590

Pro Arg Arg Ser His Gln His Gly Pro Pro Arg Gly Ala Thr Ser Phe
595 600 605

Leu Gln His Val Thr Gly His His
610 615

01997001800.ST25

<210> 9
 <211> 21
 <212> DNA
 <213> Homo sapiens

<400> 9
 aaccgcatca tcaagaacga g

21

<210> 10
 <211> 21
 <212> DNA
 <213> Homo sapiens

<400> 10
 gtcaggaaag gttagccgac t

21

<210> 11
 <211> 23
 <212> DNA
 <213> Homo sapiens

<400> 11
 agacgaaggt gcgcccattg gag

23

<210> 12
 <211> 23
 <212> DNA
 <213> Homo sapiens

<400> 12
 ctggcgatc cgaagtcaat cac

23

<210> 13
 <211> 521
 <212> DNA
 <213> Homo sapiens

<400> 13
 acgagaccac ccactactac cagctctgc tgcgcagcta ccgcctctcg ctgcaagtgg 60
 aggggaagcc ccccacgccc gtcgtggccg cagaagatgg gacccctac tactgtctgg 120
 ctgaggagaa ggaggctgcg ggtatggca gtgtggccgg cagcagcccc ttcttccgag 180
 aggagaaggc accaggtatg caaagagcca tcgaccagct ggtgacacct agtctgcagg 240
 aggctggca tgggctgtgg ggtgagacct gcaccaatgc ggtctccgac atgatggtcc 300
 ccctcaaggc agccatcact ggccaccatg tgcccgactc gggccctgag cccatcctgg 360
 cttctacag cagccgcctg gcaggccgcc acaaggcccc caagccacct gcgggttcca 420
 agtccgactc caacttcagc aacctcattc ggctgagcca ggtctcgccct gaggatgaca 480
 ggccctgccc gggcagcagc tgggaggaag gagagcatct c 521

<210> 14
 <211> 20

01997001800.ST25

<212> DNA
<213> Homo sapiens

<400> 14
acgagaccac ccactactac

20

<210> 15
<211> 20
<212> DNA
<213> Homo sapiens

<400> 15
gagatgctct ctttcctccc

20

<210> 16
<211> 1851
<212> DNA
<213> Rattus norvegicus

<220>
<221> CDS
<222> (1)..(1848)

<400> 16 atg gcc acc atc cag tca gag act gac tgt tac gac atc att gaa gtc Met Ala Thr Ile Gln Ser Glu Thr Asp Cys Tyr Asp Ile Ile Glu Val 1 5 10 15	48
ctg ggc aag ggc act ttt gga gag gtg gcc aag ggc tgg cgt cgg agt Leu Gly Lys Gly Thr Phe Gly Glu Val Ala Lys Gly Trp Arg Arg Ser 20 25 30	96
aca gga gaa atg gtg gcc atc aag atc ttg aag aac gac gcg tac cga Thr Gly Glu Met Val Ala Ile Lys Ile Leu Lys Asn Asp Ala Tyr Arg 35 40 45	144
agc cgt atc atc aag aat gag ttg aag ctg ctg cgc tgt gta cga ggc Ser Arg Ile Ile Lys Asn Glu Leu Lys Leu Leu Arg Cys Val Arg Gly 50 55 60	192
ctg gac ccc gac gag gcc cac gtc atc cgc ttc ctt gaa ttc ttc cat Leu Asp Pro Asp Glu Ala His Val Ile Arg Phe Leu Glu Phe Phe His 65 70 75 80	240
gat gcc ctc aag ttc tac ctg gtc ttt gag cta ttg gag caa aac ctc Asp Ala Leu Lys Phe Tyr Leu Val Phe Glu Leu Leu Glu Gln Asn Leu 85 90 95	288
ttt gag ttc cag aaa gag aac aac ttc gca ccc ctc cct gcc agg cac Phe Glu Phe Gln Lys Glu Asn Asn Phe Ala Pro Leu Pro Ala Arg His 100 105 110	336
atc cga act gtc aca ctg cag gtc cta aga gcg ctg gcc cgg ctc aag Ile Arg Thr Val Thr Leu Gln Val Leu Arg Ala Leu Ala Arg Leu Lys 115 120 125	384
gag ttg gct atc atc cat gct gac ctc aag cca gaa aac att atg ttg Glu Leu Ala Ile Ile His Ala Asp Leu Lys Pro Glu Asn Ile Met Leu 130 135 140	432

01997001800.ST25

gta gat cag acc cgc tgc ccc ttc agg gta aag gtg atc gac ttt ggc	480
Val Asp Gln Thr Arg Cys Pro Phe Arg Val Lys Val Ile Asp Phe Gly	
145 150 155 160	
tcg gcc agc ata ttc agt gag gtg cgc tat gtg aag gag cct tac atc	528
Ser Ala Ser Ile Phe Ser Glu Val Arg Tyr Val Lys Glu Pro Tyr Ile	
165 170 175	
cag tcc cgc ttc tac agg gcc cca gag atc ctg ttg ggg ttg ccg ttc	576
Gln Ser Arg Phe Tyr Arg Ala Pro Glu Ile Leu Leu Gly Leu Pro Phe	
180 185 190	
tgc gag aag gtg gac gtg tgg tct ctg ggc tgt gtc atg gct gag tta	624
Cys Glu Lys Val Asp Val Trp Ser Leu Gly Cys Val Met Ala Glu Leu	
195 200 205	
cac ctg ggc tgg cct ctc tac cca ggc aac aat gag tat gac cag gtg	672
His Leu Gly Trp Pro Leu Tyr Pro Gly Asn Asn Glu Tyr Asp Gln Val	
210 215 220	
cgc tac atc tgt gag acc cag ggc tta ccc aag ccc cat ctg ctg cat	720
Arg Tyr Ile Cys Glu Thr Gln Gly Leu Pro Lys Pro His Leu Leu His	
225 230 235 240	
gcg gcc cgc aag gct cac cac ttc ttc aag cgt aac ccc cac ccc gat	768
Ala Ala Arg Lys Ala His His Phe Phe Lys Arg Asn Pro His Pro Asp	
245 250 255	
gcc acc aac ccc tgg cag ctc aag tcc tct gct gac tac cta gct gag	816
Ala Thr Asn Pro Trp Gln Leu Lys Ser Ser Ala Asp Tyr Leu Ala Glu	
260 265 270	
acc aag gta cgc cca ctg gag cgc cgc aag tac atg ctc aaa tcc ttg	864
Thr Lys Val Arg Pro Leu Glu Arg Arg Lys Tyr Met Leu Lys Ser Leu	
275 280 285	
gac caa att gag acg gtg aat ggt ggc ggc gct gtg aat cgg ttg agt	912
Asp Gln Ile Glu Thr Val Asn Gly Gly Ala Val Asn Arg Leu Ser	
290 295 300	
ttt cca gac cgg gag gca ctg gcg gaa cac gcg gac ctc aag agc atg	960
Phe Pro Asp Arg Glu Ala Leu Ala Glu His Ala Asp Leu Lys Ser Met	
305 310 315 320	
gtg gag ctg atc aaa cgc atg ctg aca tgg gag tct cac gag cgc atc	1008
Val Glu Leu Ile Lys Arg Met Leu Thr Trp Glu Ser His Glu Arg Ile	
325 330 335	
agt ccc agc gcg gcc ctg cgc cac ccc ttc gtg tcc atg cag cag ctg	1056
Ser Pro Ser Ala Ala Leu Arg His Pro Phe Val Ser Met Gln Gln Leu	
340 345 350	
cgt agt gcc cac gag gcc acc cgc tac tac cag ctg tcc ctc cga ggc	1104
Arg Ser Ala His Glu Ala Thr Arg Tyr Tyr Gln Leu Ser Leu Arg Gly	
355 360 365	
tgt cgg ctg tcc ctg cag gtg gac ggc aag cca ccc cca cct gtc ata	1152
Cys Arg Leu Ser Leu Gln Val Asp Gly Lys Pro Pro Pro Pro Val Ile	
370 375 380	
gcc aac gca gag gac ggg cct ccc tac tac cgc ctg gct gag gag gag	1200
Ala Asn Ala Glu Asp Gly Pro Pro Tyr Tyr Arg Leu Ala Glu Glu Glu	
385 390 395 400	

01997001800.ST25

gag act gca ggc ctg ggt ggt gtg acc ggc agt ggg tcc ttc ttc agg Glu Thr Ala Gly Leu Gly Gly Val Thr Gly Ser Gly Ser Phe Phe Arg 405 410 415	1248
gag gac aag gct ccc gga atg cag aga gcc atc gac cag ctc gat gac Glu Asp Lys Ala Pro Gly Met Gln Arg Ala Ile Asp Gln Leu Asp Asp 420 425 430	1296
ctg agt ctg cag gag gcc cgc cgg ggg ctg tgg agc gac acg cgg gcc Leu Ser Leu Gln Glu Ala Arg Arg Gly Leu Trp Ser Asp Thr Arg Ala 435 440 445	1344
gac atg gtc tct gac atg ctg gct cca ctc aaa gta gcc act acc agc Asp Met Val Ser Asp Met Leu Ala Pro Leu Lys Val Ala Thr Thr Ser 450 455 460	1392
cat cga gtc ccc gac tcg ggc ccg gag cct atc ctg gcc ttc tac ggc His Arg Val Pro Asp Ser Gly Pro Glu Pro Ile Leu Ala Phe Tyr Gly 465 470 475 480	1440
agc cgc ttg act ggc cgc cat aag gcc cgc aag gcc cca gca ggc tcc Ser Arg Leu Thr Gly Arg His Lys Ala Arg Lys Ala Pro Ala Gly Ser 485 490 495	1488
aaa tcc gac tcc aac ttc agt aac ctc atc cgg ctg agc cag gcc tca Lys Ser Asp Ser Asn Phe Ser Asn Leu Ile Arg Leu Ser Gln Ala Ser 500 505 510	1536
cct gag gat gcg ggg tcc tgt agg ggc agt ggt tgg gaa gaa gga gaa Pro Glu Asp Ala Gly Ser Cys Arg Gly Ser Gly Trp Glu Glu Gly Glu 515 520 525	1584
ggc cac acg act tcc aca gag ccg tct gcc atc cca caa cgg gaa gga Gly His Thr Thr Ser Thr Glu Pro Ser Ala Ile Pro Gln Arg Glu Gly 530 535 540	1632
gat gga ccc agc atc aaa gac agg ccc atg gat gct gag agg tca ggc Asp Gly Pro Ser Ile Lys Asp Arg Pro Met Asp Ala Glu Arg Ser Gly 545 550 555 560	1680
cct gag ctc ttt gat ccc agc ggc tgt cct gga gag tgg cta aat gaa Pro Glu Leu Phe Asp Pro Ser Gly Cys Pro Gly Glu Trp Leu Asn Glu 565 570 575	1728
cca gaa tgg acc cta gag ggc atc cgg ggg tct cga gct caa ggg ctt Pro Glu Trp Thr Leu Glu Gly Ile Arg Gly Ser Arg Ala Gln Gly Leu 580 585 590	1776
cca gct cgc cat ccc cac cca cac ggg ccg ccc agg acc acc agc ttt Pro Ala Arg His Pro His Pro His Gly Pro Pro Arg Thr Thr Ser Phe 595 600 605	1824
ctg cag cat gtt gga ggg cac cac tga Leu Gln His Val Gly Gly His His 610 615	1851

<210> 17
 <211> 616
 <212> PRT
 <213> Rattus norvegicus

01997001800.ST25

<400> 17

Met Ala Thr Ile Gln Ser Glu Thr Asp Cys Tyr Asp Ile Ile Glu Val
1 5 10 15

Leu Gly Lys Gly Thr Phe Gly Glu Val Ala Lys Gly Trp Arg Arg Ser
20 25 30

Thr Gly Glu Met Val Ala Ile Lys Ile Leu Lys Asn Asp Ala Tyr Arg
35 40 45

Ser Arg Ile Ile Lys Asn Glu Leu Lys Leu Leu Arg Cys Val Arg Gly
50 55 60

Leu Asp Pro Asp Glu Ala His Val Ile Arg Phe Leu Glu Phe Phe His
65 70 75 80

Asp Ala Leu Lys Phe Tyr Leu Val Phe Glu Leu Leu Glu Gln Asn Leu
85 90 95

Phe Glu Phe Gln Lys Glu Asn Asn Phe Ala Pro Leu Pro Ala Arg His
100 105 110

Ile Arg Thr Val Thr Leu Gln Val Leu Arg Ala Leu Ala Arg Leu Lys
115 120 125

Glu Leu Ala Ile Ile His Ala Asp Leu Lys Pro Glu Asn Ile Met Leu
130 135 140

Val Asp Gln Thr Arg Cys Pro Phe Arg Val Lys Val Ile Asp Phe Gly
145 150 155 160

Ser Ala Ser Ile Phe Ser Glu Val Arg Tyr Val Lys Glu Pro Tyr Ile
165 170 175

Gln Ser Arg Phe Tyr Arg Ala Pro Glu Ile Leu Leu Gly Leu Pro Phe
180 185 190

Cys Glu Lys Val Asp Val Trp Ser Leu Gly Cys Val Met Ala Glu Leu
195 200 205

His Leu Gly Trp Pro Leu Tyr Pro Gly Asn Asn Glu Tyr Asp Gln Val
210 215 220

Arg Tyr Ile Cys Glu Thr Gln Gly Leu Pro Lys Pro His Leu Leu His
225 230 235 240

Ala Ala Arg Lys Ala His His Phe Phe Lys Arg Asn Pro His Pro Asp
Page 35

01997001800.ST25

245

250

255

Ala Thr Asn Pro Trp Gln Leu Lys Ser Ser Ala Asp Tyr Leu Ala Glu
260 265 270

Thr Lys Val Arg Pro Leu Glu Arg Arg Lys Tyr Met Leu Lys Ser Leu
275 280 285

Asp Gln Ile Glu Thr Val Asn Gly Gly Gly Ala Val Asn Arg Leu Ser
290 295 300

Phe Pro Asp Arg Glu Ala Leu Ala Glu His Ala Asp Leu Lys Ser Met
305 310 315 320

Val Glu Leu Ile Lys Arg Met Leu Thr Trp Glu Ser His Glu Arg Ile
325 330 335

Ser Pro Ser Ala Ala Leu Arg His Pro Phe Val Ser Met Gln Gln Leu
340 345 350

Arg Ser Ala His Glu Ala Thr Arg Tyr Tyr Gln Leu Ser Leu Arg Gly
355 360 365

Cys Arg Leu Ser Leu Gln Val Asp Gly Lys Pro Pro Pro Pro Val Ile
370 375 380

Ala Asn Ala Glu Asp Gly Pro Pro Tyr Tyr Arg Leu Ala Glu Glu Glu
385 390 395 400

Glu Thr Ala Gly Leu Gly Gly Val Thr Gly Ser Gly Ser Phe Phe Arg
405 410 415

Glu Asp Lys Ala Pro Gly Met Gln Arg Ala Ile Asp Gln Leu Asp Asp
420 425 430

Leu Ser Leu Gln Glu Ala Arg Arg Gly Leu Trp Ser Asp Thr Arg Ala
435 440 445

Asp Met Val Ser Asp Met Leu Ala Pro Leu Lys Val Ala Thr Thr Ser
450 455 460

His Arg Val Pro Asp Ser Gly Pro Glu Pro Ile Leu Ala Phe Tyr Gly
465 470 475 480

Ser Arg Leu Thr Gly Arg His Lys Ala Arg Lys Ala Pro Ala Gly Ser
485 490 495

01997001800.ST25
Lys Ser Asp Ser Asn Phe Ser Asn Leu Ile Arg Leu Ser Gln Ala Ser
500 505 510

Pro Glu Asp Ala Gly Ser Cys Arg Gly Ser Gly Trp Glu Glu Gly Glu
515 520 525

Gly His Thr Thr Ser Thr Glu Pro Ser Ala Ile Pro Gln Arg Glu Gly
530 535 540

Asp Gly Pro Ser Ile Lys Asp Arg Pro Met Asp Ala Glu Arg Ser Gly
545 550 555 560

Pro Glu Leu Phe Asp Pro Ser Gly Cys Pro Gly Glu Trp Leu Asn Glu
565 570 575

Pro Glu Trp Thr Leu Glu Gly Ile Arg Gly Ser Arg Ala Gln Gly Leu
580 585 590

Pro Ala Arg His Pro His Pro His Gly Pro Pro Arg Thr Thr Ser Phe
595 600 605

Leu Gln His Val Gly Gly His His
610 615

<210> 18
<211> 21
<212> DNA
<213> Homo sapiens

<400> 18
aagatcctca agaatgacgc c

21

<210> 19
<211> 21
<212> DNA
<213> Homo sapiens

<400> 19
aagaatgacg cctaccgcaa c

21

<210> 20
<211> 21
<212> DNA
<213> Homo sapiens

<400> 20
aaccgcatca tcaagaacga g

21

<210> 21
<211> 21
<212> DNA
<213> Homo sapiens

01997001800.ST25

<400> 21	
aagaacgagc tgaagctgct g	21
<210> 22	
<211> 21	
<212> DNA	
<213> Homo sapiens	
<400> 22	
aaggagctgg ctatcatcca c	21
<210> 23	
<211> 21	
<212> DNA	
<213> Homo sapiens	
<400> 23	
aagcctgaga acatcatgct g	21
<210> 24	
<211> 21	
<212> DNA	
<213> Homo sapiens	
<400> 24	
aacatcatgc tggtgacca g	21
<210> 25	
<211> 21	
<212> DNA	
<213> Homo sapiens	
<400> 25	
aaggtgattg acttcggatc c	21
<210> 26	
<211> 21	
<212> DNA	
<213> Homo sapiens	
<400> 26	
aaggagccat acatccagtc g	21
<210> 27	
<211> 21	
<212> DNA	
<213> Homo sapiens	
<400> 27	
aacaacgagt acgaccagg g	21
<210> 28	
<211> 21	
<212> DNA	
<213> Homo sapiens	

01997001800.ST25

<400> 28
aagtctttgg accagattga g 21

<210> 29
<211> 21
<212> DNA
<213> Homo sapiens

<400> 29
aagagcatgg tggagctgat c 21

<210> 30
<211> 21
<212> DNA
<213> Homo sapiens

<400> 30
aatgcggctt ccgacatgat g 21

<210> 31
<211> 21
<212> DNA
<213> Homo sapiens

<400> 31
aagtccgact ccaacttcag c 21

<210> 32
<211> 21
<212> DNA
<213> Homo sapiens

<400> 32
aacttcagca acctcattcg g 21

<210> 33
<211> 21
<212> DNA
<213> Homo sapiens

<400> 33
aacatgacca tggaaagctga g 21

<210> 34
<211> 21
<212> DNA
<213> Homo sapiens

<400> 34
aatggctgag tgagccagac t 21

<210> 35
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 35
gauccucaag aaugacgccc u

21

<210> 36
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 36
gaaugacgccc uaccgcaacu u

21

<210> 37
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 37
ccgcaucauc aagaacgagu u

21

<210> 38
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 38
gaacgagcug aagcugcugu u

21

<210> 39
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 39
ggagcuggcu aucauccacu u

21

<210> 40
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 40
gccugagaac aucaugcugu u 21

<210> 41
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 41
caucaugcug guggaccagu u 21

<210> 42
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 42
ggugauugac uucggauccu u 21

<210> 43
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 43
ggagccauac auccagucgu u 21

<210> 44
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 44
caacgaguac gaccaggugu u 21

<210> 45
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 45
gucguuggac cagauugagu u 21

<210> 46
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 46
gagcauggug gagcugauu u

21

<210> 47
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 47
ugcggucucc gacaugauu u

21

<210> 48
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 48
guccgacucc aacuucagcu u

21

<210> 49
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 49
cuucagcaac cucauucggu u

21

<210> 50
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 50
caugaccaug gaagcugagu u

21

<210> 51

01997001800.ST25

<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 51
uggcugagug agccagacuu u

21

<210> 52
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 52
uucuaggagu ucuuacugcg g

21

<210> 53
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 53
uucuuacugc ggauggcguu g

21

<210> 54
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 54
uuggcguagu aguucuugcu c

21

<210> 55
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 55
uucuugcucg acuucgacga c

21

<210> 56
<211> 21
<212> RNA
<213> Artificial

01997001800.ST25

<220>
<223> siRNA polynucleotide, synthesized

<400> 56
uuccucgacc gauaguagg g

21

<210> 57
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 57
uucggacucu uguaguacga c

21

<210> 58
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 58
uuguaguacg accaccuggu c

21

<210> 59
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 59
uuccacuaac ugaagccuag g

21

<210> 60
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 60
uuccucggua uguaggucag c

21

<210> 61
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 61
uuguugcuca ugcuggucca c 21

<210> 62
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 62
uucagcaacc uggucuaacu c 21

<210> 63
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 63
uucucguacc accucgacua g 21

<210> 64
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 64
uuacgccaga ggcuguacua c 21

<210> 65
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 65
uucaggcuga gguugaaguc g 21

<210> 66
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 66
uugaagucgu uggaguaagc c 21

01997001800.ST25

<210> 67
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 67
uuguacuggu accuucgacu c 21

<210> 68
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 68
uuaccgacuc acucggucug a 21

<210> 69
<211> 21
<212> DNA
<213> Homo sapiens

<400> 69
caagatcctc aagaatgacg c 21

<210> 70
<211> 21
<212> DNA
<213> Homo sapiens

<400> 70
caagaatgac gcctaccgca a 21

<210> 71
<211> 21
<212> DNA
<213> Homo sapiens

<400> 71
caaccgcattc atcaagaacg a 21

<210> 72
<211> 21
<212> DNA
<213> Homo sapiens

<400> 72
catcaagaac gagctgaagc t 21

<210> 73

01997001800.ST25

<211> 21
<212> DNA
<213> Homo sapiens

<400> 73
caagaacgag ctgaagctgc t

21

<210> 74
<211> 21
<212> DNA
<213> Homo sapiens

<400> 74
catccgcttc cttgagttct t

21

<210> 75
<211> 21
<212> DNA
<213> Homo sapiens

<400> 75
cagaaggaga acaacttcgc g

21

<210> 76
<211> 21
<212> DNA
<213> Homo sapiens

<400> 76
caaggagctg gctatcatcc a

21

<210> 77
<211> 21
<212> DNA
<213> Homo sapiens

<400> 77
caagcctgag aacatcatgc t

21

<210> 78
<211> 21
<212> DNA
<213> Homo sapiens

<400> 78
caaggtgatt gacttcggat c

21

<210> 79
<211> 21
<212> DNA
<213> Homo sapiens

<400> 79
catacatcca gtcgcgcttc t

21

<210> 80

01997001800.ST25

<211> 21
<212> DNA
<213> Homo sapiens

<400> 80
caacaacgag tacgaccagg t

21

<210> 81
<211> 21
<212> DNA
<213> Homo sapiens

<400> 81
caccaccttct tcaagcgcaa c

21

<210> 82
<211> 21
<212> DNA
<213> Homo sapiens

<400> 82
caagtcgttg gaccagattg a

21

<210> 83
<211> 21
<212> DNA
<213> Homo sapiens

<400> 83
caagagcatg gtggagctga t

21

<210> 84
<211> 21
<212> DNA
<213> Homo sapiens

<400> 84
caatgcggtc tccgacatga t

21

<210> 85
<211> 21
<212> DNA
<213> Homo sapiens

<400> 85
caagtccgac tccaacttca g

21

<210> 86
<211> 21
<212> DNA
<213> Homo sapiens

<400> 86
caacttcagc aacctcattc g

21

<210> 87

01997001800.ST25

<211> 21
<212> DNA
<213> Homo sapiens

<400> 87
caacatgacc atggaagctg a

21

<210> 88
<211> 21
<212> DNA
<213> Homo sapiens

<400> 88
catgaccatg gaagctgaga g

21

<210> 89
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 89
agaucucaa gaaugacgcu u

21

<210> 90
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 90
agaaugacgc cuaccgcaau u

21

<210> 91
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 91
accgcaucau caagaacgau u

21

<210> 92
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 92
ucaagaacga gcugaagcuh u

21

<210> 93
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 93
agaacgagcu gaagcugcuu u 21

<210> 94
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 94
uccgcuuccu ugaguucuuu u 21

<210> 95
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 95
gaaggagaac aacuucgcgu u 21

<210> 96
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 96
aggagcuggc uaucauccau u 21

<210> 97
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 97
agccugagaa caucaugcuu u 21

<210> 98

01997001800.ST25

<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 98
aggugauuga cuucggaucu u

21

<210> 99
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 99
uacauccagu cgcgcuucuu u

21

<210> 100
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 100
acaacgagua cgaccagguu u

21

<210> 101
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 101
ccacuuucuuc aagcgcaacu u

21

<210> 102
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 102
agucguugga ccagauugau u

21

<210> 103
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 103
agagcauggu ggagcugauu u

21

<210> 104
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 104
augcggucuc cgacaugauu u

21

<210> 105
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 105
aguuccgacuc caacuucagu u

21

<210> 106
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 106
acuucagcaa ccucauucgu u

21

<210> 107
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 107
acaugaccau ggaaggcugau u

21

<210> 108
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 108
ugaccaugga agcugagagu u 21

<210> 109
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 109
uuucuaggag uucuuacugc g 21

<210> 110
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 110
uuucuuacug cggauggcgu u 21

<210> 111
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 111
uuuggcguag uaguucuugc u 21

<210> 112
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 112
uuaguucuug cucgacuuucg a 21

<210> 113
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 113
uuucuugcuc gacuucgacg a 21

<210> 114
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 114
uuaggcgaag gaacucaaga a

21

<210> 115
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 115
uucuuccucu uguugaagcg c

21

<210> 116
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 116
uuuccucgac cgauaguagg u

21

<210> 117
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 117
uuucggacuc uuguaguacg a

21

<210> 118
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 118
uuuuccacuaa cugaagccua g

21

<210> 119

01997001800.ST25

<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 119
uuauaguagg u cagcgcaag a

21

<210> 120
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 120
uuuguugcuc a ugcuggucc a

21

<210> 121
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 121
uuggugaaga a guucgcguu g

21

<210> 122
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 122
uuucagcaac cuggucuaac u

21

<210> 123
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 123
uuucucguac caccucgacu a

21

<210> 124
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 124
uuuacgccag aggcuguacu a

21

<210> 125
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 125
uuucagggcug agguugaagu c

21

<210> 126
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 126
uuugaagucg uuggaguaag c

21

<210> 127
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 127
uuuguacugg uaccuucgac u

21

<210> 128
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 128
uuacugguac cuucgacucu c

21

<210> 129
<211> 21
<212> DNA
<213> Homo sapiens

<400> 129
gagatgggtgg ccatcaagat c

21

01997001800.ST25

<210> 130
<211> 21
<212> DNA
<213> Homo sapiens

<400> 130
gatggtggcc atcaagatcc t 21

<210> 131
<211> 21
<212> DNA
<213> Homo sapiens

<400> 131
gatcctcaag aatgacgcct a 21

<210> 132
<211> 21
<212> DNA
<213> Homo sapiens

<400> 132
gagttccaga aggagaacaa c 21

<210> 133
<211> 21
<212> DNA
<213> Homo sapiens

<400> 133
gatctcaagc ctgagaacat c 21

<210> 134
<211> 21
<212> DNA
<213> Homo sapiens

<400> 134
gagaacatca tgctggatgg c 21

<210> 135
<211> 21
<212> DNA
<213> Homo sapiens

<400> 135
gaacatcatg ctggatggacc a 21

<210> 136
<211> 21
<212> DNA
<213> Homo sapiens

<400> 136
gaaggagcca tacatccagt c 21

01997001800.ST25

<210> 137
<211> 21
<212> DNA
<213> Homo sapiens

<400> 137
gattgagaca gtgaatggtg g

21

<210> 138
<211> 21
<212> DNA
<213> Homo sapiens

<400> 138
gagacagtga atggcggcag t

21

<210> 139
<211> 21
<212> DNA
<213> Homo sapiens

<400> 139
gacagtgaat ggtggcagtg t

21

<210> 140
<211> 21
<212> DNA
<213> Homo sapiens

<400> 140
gagcatggtg gagctgatca a

21

<210> 141
<211> 21
<212> DNA
<213> Homo sapiens

<400> 141
gagaaggcac caggtatgca a

21

<210> 142
<211> 21
<212> DNA
<213> Homo sapiens

<400> 142
gactccaact tcagcaacct c

21

<210> 143
<211> 21
<212> DNA
<213> Homo sapiens

<400> 143
gacaacatga ccatgaaagc t

21

<210> 144
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 144
gaugguggcc aucaagaucu u

21

<210> 145
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 145
ugguggccau caagauccuu u

21

<210> 146
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 146
uccucaagaa ugacgccuau u

21

<210> 147
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 147
guuccagaag gagaacaacu u

21

<210> 148
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 148
ucucaagccu gagaacaucu u

21

<210> 149

01997001800.ST25

<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 149
gaacaaucaug cugguggacu u

21

<210> 150
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 150
acaaucaugcu gguggaccau u

21

<210> 151
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 151
aggaggccaua cauccagucu u

21

<210> 152
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 152
uugagacagu gaaugguggu u

21

<210> 153
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 153
gacagugaaau gguggcaguu u

21

<210> 154
<211> 21
<212> RNA
<213> Artificial

01997001800.ST25

<220>
<223> siRNA polynucleotide, synthesized

<400> 154
cagugaaugg uggcaguguu u 21

<210> 155
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 155
gcauggugga gcugaucaau u 21

<210> 156
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 156
gaaggccacca gguauugcaau u 21

<210> 157
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 157
cuccaacuuc agcaaccucu u 21

<210> 158
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 158
caacaugacc auggaagcuu u 21

<210> 159
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 159	21
uucuaccacc gguaguucua g	
<210> 160	
<211> 21	
<212> RNA	
<213> Artificial	
<220>	
<223> siRNA polynucleotide, synthesized	
<400> 160	21
uuaccaccgg uaguucuagg a	
<210> 161	
<211> 21	
<212> RNA	
<213> Artificial	
<220>	
<223> siRNA polynucleotide, synthesized	
<400> 161	21
uuaggaguuc uuacugcgg a	
<210> 162	
<211> 21	
<212> RNA	
<213> Artificial	
<220>	
<223> siRNA polynucleotide, synthesized	
<400> 162	21
uucaaggucu uccucuuguu g	
<210> 163	
<211> 21	
<212> RNA	
<213> Artificial	
<220>	
<223> siRNA polynucleotide, synthesized	
<400> 163	21
uuagaguucg gacucuugua g	
<210> 164	
<211> 21	
<212> RNA	
<213> Artificial	
<220>	
<223> siRNA polynucleotide, synthesized	
<400> 164	21
uucuuguagu acgaccaccu g	

<210> 165
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 165
uuuguaguac gaccaccugg u

21

<210> 166
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 166
uuuccucggu auguaggua g

21

<210> 167
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 167
uuaacucugu cacuuaccac c

21

<210> 168
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 168
uucugucacu uaccaccguc a

21

<210> 169
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 169
uugucacuua ccaccgucac a

21

<210> 170

01997001800.ST25

<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 170
uucguaccac cucgacuagu u

21

<210> 171
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 171
uucuuuccgug guccauacgu u

21

<210> 172
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 172
uugaggua ugacguugga g

21

<210> 173
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 173
uuguuguacu gguaccuucg a

21

<210> 174
<211> 21
<212> DNA
<213> Homo sapiens

<400> 174
taccgcaacc gcatcatcaa g

21

<210> 175
<211> 21
<212> DNA
<213> Homo sapiens

<400> 175
tacgtgaagg agccatacat c

21

<210> 176
<211> 21
<212> DNA
<213> Homo sapiens

<400> 176
tacatccagt cgcgcttcta c

21

<210> 177
<211> 21
<212> DNA
<213> Homo sapiens

<400> 177
tatgctcaag tcgttggacc a

21

<210> 178
<211> 21
<212> DNA
<213> Homo sapiens

<400> 178
tactactgtc tggctgagga g

21

<210> 179
<211> 21
<212> DNA
<213> Homo sapiens

<400> 179
tactgtctgg ctgaggagaa g

21

<210> 180
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 180
ccgcaaccgc aucaucaagu u

21

<210> 181
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 181
cgugaaggag ccauacaucu u

21

<210> 182

01997001800.ST25

<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 182
cauccagucg cgcuucuacu u

21

<210> 183
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 183
ugcucaaguc guuggaccau u

21

<210> 184
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 184
cuacugucug gcugaggagu u

21

<210> 185
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 185
cugucuggcu gaggagaagu u

21

<210> 186
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 186
uuggcguugg cguaguaguu c

21

<210> 187
<211> 21
<212> RNA
<213> Artificial

01997001800.ST25

<220>
<223> siRNA polynucleotide, synthesized

<400> 187
uugcacuucc ucgguaugua g

21

<210> 188
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 188
uuguaggua gcgcgaagau g

21

<210> 189
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 189
uuacgaguuc agcaaccugg u

21

<210> 190
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 190
uugaugacag accgacuccu c

21

<210> 191
<211> 21
<212> RNA
<213> Artificial

<220>
<223> siRNA polynucleotide, synthesized

<400> 191
uugacagacc gacuccucuu c

21